

79477

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From: Ibrahim, Medina A.
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Medina A. Ibrahim
Patent Examiner
GAU:1638
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PAUL SCHULWITZ
TECHNICAL INFO. SPECIALIST
CM1 6B06 TEL. (703) 305-1954

Searcher: _____
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Online time: 10

TYPE OF SEARCH:
NA Sequences: 1
AA Sequences: _____
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Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
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DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

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OM nucleic - nucleic search, using sw model
Run on: November 12, 2002, 02:19:04 ; Search time 5092 Seconds
(without alignments)
11025.002 Million cell updates/sec

Title: US-09-771-045A-35
Perfect score: 1929
Sequence: 1 atggcacttgaccagagcta.....gcttggtgccgcagcatag 1929

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:
1: gb_ba.*
2: gb_htg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
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11: gb_sts.*
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33: em_htg_mus.*
34: em_htg_pln.*
35: em_htg_rtd.*
36: em_htg_mam.*
37: em_htg_wrt.*
38: em_sy.*
39: em_htgo_hum.*
40: em_htgo_mus.*
41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query % | Match | Length | DB | ID | Description |
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| 1 | 1929 | 100.0 | 1929 | 6 | ARI45464 | ARI45464 | Sequence |
| 2 | 1929.8 | 99.8 | 1929 | 6 | ARI45465 | ARI45465 | Sequence |
| 3 | 1851.4 | 96.0 | 1930 | 6 | ARI45466 | ARI45466 | Sequence |
| 4 | 1792.2 | 92.9 | 1928 | 6 | ARI45468 | ARI45468 | Sequence |
| 5 | 1789 | 92.7 | 1928 | 6 | ARI45469 | ARI45469 | Sequence |
| 6 | 1787.4 | 92.7 | 1928 | 6 | ARI45467 | ARI45467 | Sequence |
| 7 | 1602.6 | 83.1 | 1803 | 6 | ARI45457 | ARI45457 | Sequence |
| 8 | 1602.6 | 83.1 | 1803 | 6 | ARI45484 | ARI45484 | Sequence |
| 9 | 1596.2 | 82.7 | 2490 | 6 | ARI45462 | ARI45462 | Sequence |
| 10 | 1596.2 | 82.7 | 2490 | 6 | ARI45489 | ARI45489 | Sequence |
| 11 | 1319 | 68.4 | 1442 | 6 | ARI45448 | ARI45448 | Sequence |
| 12 | 1319 | 68.4 | 1442 | 6 | ARI45475 | ARI45475 | Sequence |
| 13 | 1212.2 | 62.8 | 2976 | 6 | ARI45459 | ARI45459 | Sequence |
| 14 | 1212.2 | 62.8 | 2976 | 6 | ARI45486 | ARI45486 | Sequence |
| 15 | 1212.2 | 62.8 | 3003 | 6 | ARI45458 | ARI45458 | Sequence |
| 16 | 1212.2 | 62.8 | 3003 | 6 | ARI45485 | ARI45485 | Sequence |
| 17 | 1212.2 | 62.8 | 3591 | 6 | ARI45461 | ARI45461 | Sequence |
| 18 | 1212.2 | 62.8 | 3591 | 6 | ARI45488 | ARI45488 | Sequence |
| 19 | 1212.2 | 62.8 | 3618 | 6 | ARI45460 | ARI45460 | Sequence |
| 20 | 1212.2 | 62.8 | 3618 | 6 | ARI45487 | ARI45487 | Sequence |
| 21 | 1212.2 | 62.8 | 1392 | 6 | ARI45449 | ARI45449 | Sequence |
| 22 | 1212.2 | 62.8 | 1392 | 6 | ARI45476 | ARI45476 | Sequence |
| 23 | 1212.2 | 62.8 | 1464 | 6 | ARI45456 | ARI45456 | Sequence |
| 24 | 1212.2 | 62.8 | 1464 | 6 | ARI45483 | ARI45483 | Sequence |
| 25 | 1212.2 | 62.8 | 1673 | 6 | ARI45454 | ARI45454 | Sequence |
| 26 | 1212.2 | 62.8 | 1673 | 6 | ARI45481 | ARI45481 | Sequence |
| 27 | 1212.2 | 62.8 | 2079 | 6 | ARI45455 | ARI45455 | Sequence |
| 28 | 1212.2 | 62.8 | 2079 | 6 | ARI45482 | ARI45482 | Sequence |
| 29 | 1211 | 62.8 | 1389 | 6 | ARI45447 | ARI45447 | Sequence |
| 30 | 1211 | 62.8 | 1389 | 6 | ARI45474 | ARI45474 | Sequence |
| C 31 | 361.4 | 18.7 | 372 | 6 | ARI45443 | ARI45443 | Sequence |
| C 32 | 361.4 | 18.7 | 372 | 6 | ARI45470 | ARI45470 | Sequence |
| C 33 | 174 | 9.0 | 182 | 6 | ARI45444 | ARI45444 | Sequence |
| C 34 | 174 | 9.0 | 182 | 6 | ARI45471 | ARI45471 | Sequence |
| C 35 | 51.4 | 2.7 | 31360 | 1 | SC9C7 | SC9C7 | Sequence |
| C 36 | 49.8 | 2.6 | 30650 | 1 | SME591783 | SME591783 | Sequence |
| C 37 | 48.6 | 2.5 | 125020 | 9 | AF429315 | AF429315 | Homo sapi |
| C 38 | 46.6 | 2.4 | 125020 | 9 | AF429315 | AF429315 | Homo sapi |
| C 39 | 44.6 | 2.3 | 1715 | 4 | AB038563 | AB038563 | Canis fam |
| C 40 | 44.4 | 2.3 | 715 | 11 | PM1H6G | PM1H6G | Canis fam |
| C 41 | 43.8 | 2.3 | 1795 | 4 | BTMAOA | BTMAOA | Canis fam |
| C 42 | 41.8 | 2.2 | 661 | 1 | AF230492 | AF230492 | Bovine MRNA |
| C 43 | 41.8 | 2.2 | 31624 | 1 | SCD63 | SCD63 | Streptomy |
| C 44 | 41 | 2.1 | 349498 | 1 | AP003002 | AP003002 | Mesorhizo |
| C 45 | 40.8 | 2.1 | 1560 | 9 | S62734 | S62734 | monoamine o |

ALIGNMENTS

RESULT 1
ARI45464
LOCUS ARI45464
DEFINITION Sequence 35 from patent US 6211434.
ACCESSION ARI45464
VERSION ARI45464.1 GI:15107331
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1929)
AUTHORS Duvick,J.P., Gillingham,J.T. and Maddox,J.R.
TITLE Amino polyol amine oxidase polynucleotides and related polypeptides
and methods of use
JOURNAL Patent: US 6211434-A 35 03-APR-2001;

| FEATURES | | Location/Qualifiers | |
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| source | 1. .1929 | | |
| BASE COUNT | | 451 a | 537 c 532 g 409 t |
| ORIGIN | | | |
| Query Match 100.0%; Score 1929; DB 6; Length 1929; | | | |
| Best Local Similarity 100.0%; Pred. No. 0; | | | |
| Matches 1929; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | | | |
| QY | 1 | ATGGCACTTGCACCGAGCTACATCAATCCCGCAAGCTCGCCCTCCCGCAGCAGGATATCC | 60 |
| Db | 1 | ATGGCACTTGCACCGAGCTACATCAATCCCGCAAGCTCGCCCTCCCGCAGCAGGATATCC | 60 |
| QY | 61 | CACATCGGCGTAGGCGCCAAAGCAAGCGAGGTATGTGACAAATAGCTGGACAGATTGGACAA | 120 |
| Db | 61 | CACATCGGCGTAGGCGCCAAAGCAAGCGAGGTATGTGACAAATAGCTGGACAGATTGGACAA | 120 |
| QY | 121 | GAGCGTTTGGCGGTGACAGACCCAGCCTACGAGAAACAGGTTGCCCAAGCATTCGCCAAT | 180 |
| Db | 121 | GAGCGTTTGGCGGTGACAGACCCAGCCTACGAGAAACAGGTTGCCCAAGCATTCGCCAAT | 180 |
| QY | 181 | CTCGGAGCTTGCCCTTGCTGCTGAGTGGAGCCTCTTCAAGCAGCTCACCAAGCTCAATTAC | 240 |
| Db | 181 | CTCGGAGCTTGCCCTTGCTGCTGAGTGGAGCCTCTTCAAGCAGCTCACCAAGCTCAATTAC | 240 |
| QY | 241 | TACATCGTGCAGTACGCGCCGAGCAAACTCACGCGAATGGAGATGGGTGAAGTCTACCT | 300 |
| Db | 241 | TACATCGTGCAGTACGCGCCGAGCAAACTCACGCGAATGGAGATGGGTGAAGTCTACCT | 300 |
| QY | -301 | TTTGGCCCTTGACAGGCTCCCTCCTTGACAGCTGGTGCAGCTACCGGCCCTTGGCTTCACCT | 360 |
| Db | 301 | TTTGGCCCTTGACAGGCTCCCTCCTTGACAGCTGGTGCAGCTACCGGCCCTTGGCTTCACCT | 360 |
| QY | 361 | GAATACCTCTTTGAGGTTGATGCCACGGCGTGGTGGCCAGGACATCGACCCGAGCAAC | 420 |
| Db | 361 | GAATACCTCTTTGAGGTTGATGCCACGGCGTGGTGGCCAGGACATCGACCCGAGCAAC | 420 |
| QY | 421 | GTTGGCGAGCTGGTATGGTGGCGCTGGCTTGAGCGGTTTGAGAGACGGCAGCAAGTGC | 480 |
| Db | 421 | GTTGGCGAGCTGGTATGGTGGCGCTGGCTTGAGCGGTTTGAGAGACGGCAGCAAGTGC | 480 |
| QY | 481 | CAGGCGCGGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT | 540 |
| Db | 481 | CAGGCGCGGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT | 540 |
| QY | 541 | CTGAGCGTACAAATCGGCTCCCGGAGGACGACTATCAACGACCTCGGCGCTCGGTGGATC | 600 |
| Db | 541 | CTGAGCGTACAAATCGGCTCCCGGAGGACGACTATCAACGACCTCGGCGCTCGGTGGATC | 600 |
| QY | 601 | AATGACAGCAACCAAGCGAAGTATCCAGATTTGTTGAAGATTTTCATTTGGAGGCGGAG | 660 |
| Db | 601 | AATGACAGCAACCAAGCGAAGTATCCAGATTTGTTGAAGATTTTCATTTGGAGGCGGAG | 660 |
| QY | 661 | CTCCAGAGGACGACCGGAAATTCATCCATCAAGCAGCAGCTACACCTACAGCT | 720 |
| Db | 661 | CTCCAGAGGACGACCGGAAATTCATCCATCAAGCAGCAGCTACACCTACAGCT | 720 |
| QY | 721 | CCTTATGTTGACTCCCGGTAAAGCACAATCCCACTTTGTTGATGAGACCTCTCTGCGAGTGT | 780 |
| Db | 721 | CCTTATGTTGACTCCCGGTAAAGCACAATCCCACTTTGTTGATGAGACCTCTCTGCGAGTGT | 780 |
| QY | 781 | AGAATACAGTCACTGACTCCACTTCTGCTGAGCTGAGCGGAGGAGTTGCAAGTGCACATTGC | 840 |
| Db | 781 | AGAATACAGTCACTGACTCCACTTCTGCTGAGCTGAGCGGAGGAGTTGCAAGTGCACATTGC | 840 |
| QY | 841 | GGAAGCTCTCCCGGTATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT | 900 |
| Db | 841 | GGAAGCTCTCCCGGTATGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT | 900 |
| QY | 901 | GAGCCCTCAGGCGAAGCGGCTCGACGTTGAGCTTCGCGCACTACTGTGAGAAGGACCT | 960 |
| Db | 901 | GAGCCCTCAGGCGAAGCGGCTCGACGTTGAGCTTCGCGCACTACTGTGAGAAGGACCT | 960 |

RESULT 2

AR145465

LOCUS

AR145465

1929 bp

DNA

linear

PAT 08-AUG-2001

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| Db | 961 | AAACTTGCCTGCTGTTCTCAGCTGGCAAAACAGATCACACGGGCTCTGCTCGGTGTGGA 1020 |
| QY | 1021 | AGCCACAGAGATCAGCATGCTTTTCTCACCAGCTACATCAAGAGTGGCCACCGGTCTCAG 1080 |
| Db | 1021 | AGCCACAGAGATCAGCATGCTTTTCTCACCAGCTACATCAAGAGTGGCCACCGGTCTCAG 1080 |
| QY | 1081 | TATATTGTCTCGGACAAAGAGCGGGCAGTATATGATGCAAAACAGTGGCGTG 1140 |
| Db | 1081 | TATATTGTCTCGGACAAAGAGCGGGCAGTATATGATGCAAAACAGTGGCGTG 1140 |
| QY | 1141 | CGGTGCTCTCAGTAGGGGACTGTTTCTTACTGGTCAATCCAGGTATGCAAGTCAAT 1200 |
| Db | 1141 | CGGTGCTCTCAGTAGGGGACTGTTTCTTACTGGTCAATCCAGGTATGCAAGTCAAT 1200 |
| QY | 1201 | TGCCATGCCATGTCAAAGAACTTGTCCAGGCTCAGTGACCTCAACACCCCGCTCGCT 1260 |
| Db | 1201 | TGCCATGCCATGTCAAAGAACTTGTTCAGGCTCAGTGACCTCAACACCCCGCTCGCT 1260 |
| QY | 1261 | GGAATTGAGCAGTCCGGCTGCTATAGTACGACGCTCGGGCGCGTGGTCCGA 1320 |
| Db | 1261 | GGAATTGAGCAGTCCGGCTGCTATAGTACGACGCTCGGGCGCGTGGTCCGA 1320 |
| QY | 1321 | AGCAAAAGGTTGGTTCGTTACCCGACACATGTATCCACCTTGACATTTTCAACA 1380 |
| Db | 1321 | AGCAAAAGGTTGGTTCGTTACCCGACACATGTATCCACCTTGACATTTTCAACA 1380 |
| QY | 1381 | CTCTTCCCGCGGAGCAAGCAAGCAATTTGGGAAAATCTATCTCGGCTACTATAGCAAG 1440 |
| Db | 1381 | CTCTTCCCGCGGAGCAAGCAAGCAATTTGGGAAAATCTATCTCGGCTACTATAGCAAG 1440 |
| QY | 1441 | ATAGTCTCGTATGGGACAAACCCGTGGTGGCGGCGAAACAGGCTTCTCGGGCGTCTCCAA 1500 |
| Db | 1441 | ATAGTCTCGTATGGGACAAACCCGTGGTGGCGGCGAAACAGGCTTCTCGGGCGTCTCCAA 1500 |
| QY | 1501 | TCCAGCTGTGAGCCCATCTCATTTGCCAGAGATACCAAGTCCGATCGGCAATGG 1560 |
| Db | 1501 | TCCAGCTGTGAGCCCATCTCATTTGCCAGAGATACCAAGTCCGATCGGCAATGG 1560 |
| QY | 1561 | TCCATTAACCTGTTTCATGTTGGAGACCCGGAGCGGAGTGGTCCCAAGTCCCAAGCAG 1620 |
| Db | 1561 | TCCATTAACCTGTTTCATGTTGGAGACCCGGAGCGGAGTGGTCCCAAGTCCCAAGCAG 1620 |
| QY | 1621 | GTACGACAAAGTCTGTCTGGGACCACTCCGCGCAGCTACGAGAACCGCGGCGCCAA 1680 |
| Db | 1621 | GTACGACAAAGTCTGTCTGGGACCACTCCGCGCAGCTACGAGAACCGCGGCGCCAA 1680 |
| QY | 1681 | GTCCAGAGCCGGCCAAAGTGTCTGAAATCGAGTGGTGGAGAGAGATATTTCCAAGGA 1740 |
| Db | 1681 | GTCCAGAGCCGGCCAAAGTGTCTGAAATCGAGTGGTGGAGAGAGATATTTCCAAGGA 1740 |
| QY | 1741 | GCTCCGAGCGCGTCTATGGGTGAACGATCTCATCACTGGGTTCGGCGCTCAGAAGC 1800 |
| Db | 1741 | GCTCCGAGCGCGTCTATGGGTGAACGATCTCATCACTGGGTTCGGCGCTCAGAAGC 1800 |
| QY | 1801 | CCGTTCAAGTGTGTTCAATTCGTTGGAACGAGAGCTCTTTAGTTTGGAAAGGATATAG 1860 |
| Db | 1801 | CCGTTCAAGTGTGTTCAATTCGTTGGAACGAGAGCTCTTTAGTTTGGAAAGGATATAG 1860 |
| QY | 1861 | GAAGGGCCATACGATCGGGTCAACGAGGTGCTCAGAGTGTGGCTAGCCTGGTGCCA 1920 |
| Db | 1861 | GAAGGGCCATACGATCGGGTCAACGAGGTGCTCAGAGTGTGGCTAGCCTGGTGCCA 1920 |
| QY | 1921 | GCAGCATAG 1929 |
| Db | 1921 | GCAGCATAG 1929 |

QY 1861 GAAGGGCCATACGATCGGCTCAACGAGGTGCTGCAGAGTTGTGCTAGCCTGGTGCCA 1920
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Db 1861 GAAGGGCCATACGATCGGCTCAACGAGGTGCTGCAGAGTTGTGCTAGCCTGGTGCCA 1920
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QY 1921 GCAGCATAG 1929
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Db 1921 GCAGCATAG 1929
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RESULT 3
AR145466
LOCUS AR145466 1930 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 39 from patent US 6211434.
ACCESSION AR145466
VERSION AR145466.1 GI:15107333
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1930)
AUTHORS DuVick,J.P., Gilliam,J.T. and Maddox,J.R.
TITLE Amino polyol amine oxidase polynucleotides and related polypeptides
and methods of use
JOURNAL Patent: US 6211434-A 39 03-APR-2001;
FEATURES Location/Qualifiers
#source 1..1930
BASE COUNT 449 a 531 c 537 g 412 t 1 others
ORIGIN
Query Match 96.0%; Score 1851.4; DB 6; Length 1930;
Best Local Similarity 97.8%; Pred. No. 0;
Matches 1887; Conservative 0; Mismatches 42; Indels 1; Gaps 1;
QY 1 ATGGCAGTTGACCGAGCTACATCAATCCCCCAACGTCGCTCCCGAGCGGTTATTCC 60
Db 1 ATGGCAGTTGACCGAGCTACATCAATCCCCCAACGTCGCTCCCGAGCGGTTATTCT 60
QY 61 CACATCGGCGTAGGCCCCAACGAAGCGAGGTATGTGACAATAGCTGGACAGATTGGACAA 120
Db 61 CAGTCGGCGTAGGCCCCAGACGAGGAGGTATGTGACANTAGCTGGACAGATTGGACAA 120
QY 121 GAGCCTTTGGGCGTGACAGACCCAGCTACGAGAACAGGTGGCCCAAGCATTCGCCAAT 180
Db 121 GAGCCTTCGGGCGTGACAGACCCAGCTACGAGAACAGGTGGCCCAAGCATTCGCCAAT 180
QY 181 CTGCGAGCTTGCTTGCTGCTGACGTGAGGCTCTTCAACGAGGCTCACCAAGCTCAATTAC 240
Db 181 CTGCGAGCTTGCTTGCTGCTGAGGCTCTTCAACGAGGCTCACCAAGCTCAATTAC 240
QY 241 TACATCGTCTAGTACGCGCGAGCAAACTCACCGCAATTGGAGATGGGCTGAAGTCTACC 300
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Db 301 TTTGCCCTTGACAGGCTCCCTCTTGACGCTGGTGCCAGTACCAGGCTTGCGCTTCACT 360
QY 361 GAATACCTCTTTGAGTTGATCCACGCGGCTGGCTTGAGCGGTTTGGAGACGCGACGAAAGTC 420
Db 361 GAATACCTCTTTGAGTTGATCCACGCGGCTGGCTTGAGCGGTTTGGAGACGCGACGAAAGTC 420
QY 421 GTTGGGAGCTGGTATGTTGGGCGCTGGCTTGAGCGGTTTGGAGACGCGACGAAAGTC 480
Db 421 GTTGGGAGCTGGTATGTTGGGCGCTGGCTTGAGCGGTTTGGAGACGCGACGAAAGTC 480
QY 481 CAGGCGCGCGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
Db 481 CAGGCGCGCGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
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QY 601 AATCACAGCAACCAAGCGAAGTATCCAGATTTGTTTGAAGATTTTCATTTGGAGGGCGAG 660
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Db 601 AATCACAGCAACCAAGCGAAGTATCCAGATTTGTTTGAAGATTTTCATTTGGAGGGCGAG 660
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Db 661 CTCAGAGGACGACTGGAAATTCATCCATCAAGCAACAGACGGTACAACTACAGCT 720
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QY 781 AGAATACAGTCACTGACTCCACTTCGTCAGCTGAGGAGGAGTTCGAAGTGCACCTTGC 840
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Db 781 AGAATACAGTCACTGATTCCTGTCAGCTGAGGAGGAGTTCGAAGTGCACCTTGC 840
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Db 841 GGAATCTCTCCCGTATGGTCTCAGCTGATCGAAGAGTATAGCCTTCAAGACCTCAAGGC 900
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Db 1081 TAATATTTCTCGGACAAAGAACGCGGCGAGTATATCGGATGCAAAACAGGTGCGTG 1140
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QY 1260 TGAATTTGACGAGTCGGGCTCGGCTGTAGTACGATCGGCTCGGCGCGCTGTTCCG 1319
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Db 1261 TGAATTTGACGAGTCGGGCTCGGCTGTAGTACGATCGGCTCGGCGCGCTGTTCCG 1320
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QY 1320 AAGCAAAAGTGGTGGTTTTCGTTACCGCAACATTTGATCCACCTTGACATTTTCAAC 1379
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Db 1321 AAGCAAAAGTGGTGGTTTTCGTTACCGCAACCTTTGATCCACCTTGACATTTTCAAC 1380
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QY 1380 ACTTCTCCCGCGAGAAAGCAAGCATTTGGCGGAAATATCTCTCGGCTACTATAGCAA 1439
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QY 1440 GATAGTCTGATGGGACAAACCGTGGTGGCGGACAGGCTTCTCGGCGCTCTCCA 1499
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QY 1920 AGCAGCATAG 1929
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Db 1921 AGCAGCATAG 1930
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RESULT 4
AR145468
LOCUS AR145468 1928 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 43 from patent US 6211434.
ACCESSION AR145468
VERSION AR145468.1 GI:15107335
KEYWORDS
SOURCE
ORGANISM
Unknown.
REFERENCE
Unclassified.
1 (bases 1 to 1928)
AUTHORS Duwick,J.P.; Galliam,J.T. and Maddox,J.R.
TITLE Amino polyol amine oxidase polynucleotides and related polypeptides
and methods of use
JOURNAL Patent: US 6211434-A 43 03-APR-2001;
FEATURES Location/Qualifiers
source 1..1928
BASE COUNT 450 a 527 c 534 g 417 t
ORIGIN

Query Match 92.9%; Score 1792.2; DB 6; Length 1928;
Best Local Similarity 95.9%; Pred. No. 0;
Matches 1850; Conservative 0; Mismatches 78; Indels 1; Gaps 1;

QY 1 ATGGCAGTTGCACCGAGCTACATCAATCCCAACAGCTCGCCTCCCGCAGCGGTATTCC 60
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Db 1 ATGGCAGTTGCACCGAGCTACATCAATCCCAACAGCTCGCCTCCCGCAGCGGTATTCC 60
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QY 61 CACATCGCGGTAGGCCCAACAGCAGAGGTATGTGACAATAGCTGGACAGATTGGACAA 120
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Db 61 TAGCTGCGCGTAGGCCCAACAGCAGAGGTATGTGACAATAGCTGGACAGATTGGACAA 120
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QY 121 GAGCGTTTGGGCGTGACAGACCGACCTACGAGAAACAGGTGTGCCAAGCAATTCGCCAAT 180
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Db 121 GAGCGTTGCGGCGTGACAGACCGCTGCCCTACGAGAAACAGGTGTGCCAAGCAATTCGCCAAC 180
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QY 181 CTGCGAGCTTGGCTGTGTCAGTGTGAGGCTCTTCAACAGCAGCTCACCAGCTCAATTAC 240
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Db 181 CTGCGAGCTTGTCTGTGTCAGTGTGAGGCTCTTCAACAGCAGCTTACCAAGCTCAATTAC 240
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QY 241 TACATCGTCACTACGCCCGCAGCAAACTCACCGCAATTTGGAGATGGGCTGAAGTCTACC 300
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Db 241 TACATCGTCACTACACCCGAGCAAACTCACCGCAATTTGGAGATGGGCTGAAGGCTACC 300
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QY 301 TTTGCCCTTGACAGGCTCCCTCTTTCAGCGTGTGGTCCAGTACCGGCTTGGCTTCACCT 360
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Db 301 TTTGCCCTTGACAGGCTCCCTCTTTCAGCGTGTGGTCCAGTACCGGCTTGGCTTCACCT 360
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QY 361 GAATACCTCTTTAGGTTGATGCCAGGGCGTGGTGCCAGGACACTCGACCCCAAGACAA 420
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Db 361 GAATACCTCTTTAGGTTGATGCCAGGGCGTGGTTCCAGGACACTCAACCCCAAGACAA 420
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QY 421 GTTGGGAGCGTGTAGTGTGGCGCTGGCTTGAGCGGTTTGGAGACGGCACGCAAAAGTC 480
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Db 421 GTTGGGAGCGTGTAGTGTGGCGCTGGCTTGAGCGGTTTGGAGACGGCACGCAAAAGTC 480
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QY 481 CAGGCGCGCGGTCTGTCTCTGCTCGTTCTTGAAGCGATGAGATCGTGTAGGGGGGAAAGACT 540
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Db 481 CAGGCTGCGGCGCTGTCTGCTCGTTCTTGAAGCGATGAGATCGTGTAGGGGGGAAAGACT 540
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QY 541 CTGACCGTACATCGGTTCCCGGAGGAGGACGACTATCAACGACCTCGGCGCTGCGTGGATC 600
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Db 541 CTGACCGTACATCGGTTCCCGGAGGAGGACGACTATCAATGACCTCGGCGCTGCGTGGATC 600
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QY 601 AATGACAGCAACCAAGCGAAGTATCCAGATGTGTTGAAAGATTTCAATTTGAGGGCGAG 660
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Db 601 AATGACAGCAACCAAGCGAAGTATTCAAATTAATTTGAAAGATTTCAATTTGAGGGCGAG 660
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QY 661 CTCCAGAGGACGACCGGAAATTCATTCATCAAGCACAAGAGGGTACAACTACAGCT 720
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Db 661 CTCCAGAGGACGACCGGAAATTCATTCATCAAGCACAAGAGGGTACAACTACAGCT 720
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Db 781 AGAATACAGTCTGACTCCACATCGTCAGCTGAGCGAGGAGTTGCAAGTGCACCTTGC 840
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QY 841 GGAATCTCCCGGTATGTTCTCAGCTGATCGAAGATATAGCCTTGAAGACCCCAAGGC 900
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Db 961 AAATTTGCTGCTGTGTTCTCGGCGTGGCAAAACAGATACACCGGCTCTGCTCGGTGTGA 1020
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QY 1021 AGCCACGAGATCAGCATGCTTTTCTACCGCACTACATCAAGAGTGCACCGGCTCTCAG 1080
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Db 1021 AGCCACGAGATCAGCATGCTTTTCTACCGCACTACATCAAGAGTGCACCGGCTCTCAG 1080
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Db 1081 TAATATTGCTCGATAGAAAGACCGGTGGCAGTATATCGATGCAAAACAGGTGCGTG 1140
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QY 1141 CGGTGCTCTCAGGTAGGGAGCTCGTTCTTAGTGGTCAATTCAGGTATGAGTGCATT 1200
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Db 1141 TGTGTTCTCTCA-GTGGGAGACTCGTTTCTTAGTGGTCAATTCAGGTATGAGTGCATT 1199
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QY 1201 TGCATGCCATGTCAAGAGCACTTGTTCAGGCTCAGTGCACCTCAACCCCGCTCGCT 1260
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Db 1200 TGCATGCCATGTCAAGAGCACTTGTTCAGGCTCAGTGCACCTCAACCCCGCTCGCT 1259
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QY 1261 GGAATTGAGCAGTGGCGCTCCGCTGTATAGTACGATCGGCGCTCGGCGCGCTGTTCCGA 1320
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Db 1260 GAATTTGAGCAGTGGCATCCGCTGTACAGTACGATCGGCTCGGCGCGCTGTTCCGA 1319
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QY 1321 AGCAAAAGGTGTTGTTTACCGCAACATTTGATCCCACTTGACATTTTCACCA 1380
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Db 1320 AGTAAAAAGGTGTTGTTTACCGCAACCTTGTATCCCACTTGATATTTTCACCA 1379
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QY 1381 CCTCTTCCCGCAGAGCAGCATTTGGCGGAAAAATCTATCTCGCTACTATAGCAAG 1440
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QY 1441 ATAGTCTTCGTATGGGACAACCCCGTGTGGCGGAAACAGGCTTCTGGGCGCTCTCCAA 1500
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Db 1440 ATAGTCTTCGTATGGGACAACCCCGTGTGGCGGAAACAGGCTTCTGGGCGCTCTCCAA 1499
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QY 1501 TCAGAGTGTGACCCCAATCTCATTTTCCAGAGATACCAAGCATCGAAGTCGATCGCAATGG 1560
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QY 1621 GTACGACAAAAGTCTGTCTGGGACCAACTCCGCGCAGCCCTACGAGAACGCCGGGGCCAA 1680
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Db 1620 GTACGACAGAAGTCTGTCTGGAACCAACTCCGCGCAGCCCTACGAGAACGCCGGGGCCAA 1679
QY 1681 GTCCAGAGCCGGCCCAAGCTGCTGGAATCGAGTGGTCGAAGCAGCAGTATTTCCRAGGA 1740
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Db 1680 GTCCAGAGCCGGCCCAAGCTGCTCGAGATCGAGTGGTCGAAGCAGCAGTATTTCCRAGGA 1739
QY 1741 GCTCCGAGCGCGCTATGTGGCTGAACCATCTCATCACACTGGGTTCGGCGCTCAGAACG 1800
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Db 1740 GCGCGAGCGCGCTATGTGGCTGAACCTGTCTCAACACACTGGGTTCGGCGCTCAGAACG 1799
QY 1801 CCGTTCAGTGTGTCATTTGTTGGAAACGAGACAGCTCTTTAGTTGGAAAGGTTATATG 1860
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Db 1800 CCGTTCAGGTTGTTCAATTTCTGTTGGAACGAGACAGCTCTTTGGTTTGGAAAGGTTATATG 1859
QY 1861 GAAGGGGCATACGATCGGGTCAACAGAGTCTGCAGAAAGTTGTGGCTAGCCTGGTGCCA 1920
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Db 1860 GAAGGGGCATACGATCGGGTCAGGAGGCGCTGCAGAAAGTTGTGGCTAGCCTGGTGCCA 1919
QY 1921 GCAGCATAG 1929
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Db 1920 GCAGCATAG 1928

RESULT 5
AR145469
LOCUS AR145469 1928 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 45 from patent US 6211434.
ACCESSION AR145469
VERSION AR145469.1 GI:15107336
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1928)
AUTHORS Duwick,J.P.; Gilliam,J.T. and Maddox,J.R.
TITLE Amino polyol amine oxidase polynucleotides and related polypeptides
and methods of use
JOURNAL Patent: US 6211434-A 45 03-APR-2001;
FEATURES Location/Qualifiers
source 1. 1928
BASE COUNT 449 a 528 c 534 g 417 t
ORIGIN

Query Match 92.7%; Score 1789; DB 6; Length 1928;
Best Local Similarity 95.8%; Pred. No. 0;
Matches 1848; Conservative 0; Mismatches 80; Indels 1; Gaps 1;

QY 1 ATGGCACTTGCACGAGCTACATCAATCCCCCAACAGTCGCTCCCGCAGCAGGGTATTCC 60
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Db 61 CACGTCGGCGTAGGCCCAACGAAGCGAGGTATGTGACAATAGCTGGACAGATTGGACAA 120
QY 121 GACGCTTTGGGGCTGACAGACCCAGCCTACGAGAAACAGGTTGCCCAAGCAATTGCGCAAT 180
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QY 181 CTGCGAGCTTGCCTTGTGCTGAGTGGAGCCCTTCAACAGACGTCACCAAGCTCAATTAC 240
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Db 181 CTGCGAGCTTGTCTGTGCTGAGTTGGAGCCACTTCAACAGCATTACCAAGCTCAATTAC 240

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QY 361 GAATACCTCTTTGAGGTGTGATGCCACGCGCTGGTGCCAGGACACTCGACCCCGACAAAC 420
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QY 421 GTTGGGAGAGTGTGATGGTGGGCGCTGGCTTGAGCGGTTTGGAGAGCGGACCCAAAGTC 480
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Db 421 GTTGGGAGAGTGTGATGGTGGGCGCTGGCTTGAGCGGTTTGGAGAGCGGACCCAAAGTC 480
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QY 541 CTGAGCGTACAAATCGGGTCCCGGAGGACGACTATCAACGACCTCGGCGTGGTGGAATC 600
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QY 601 AATGACAGCAACCAAGCGAAGTATCCAGATTTGTTTGAAGAATTTCAATTTGAGAGGCGGAG 660
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QY 721 CCTATGCTGACTCCCGGTGAAGCACAATCCCACTTTGTGATGAGACCTCTGTCGAGTGT 780
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QY 841 GGAACCTCTCCCGCTATGCTCAGCTGATCGAAGAGTATAGCTTTGAAGACCCCAAGGC 900
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Db 841 GGAACCTCTCCCGCATGGTCTCAGCTGATCGAAGAGCATAGTCTTGAAGACCCCAAGGC 900
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Db 1021 AGCCACAGATACAGCATGCTTTTCTCACCGCATACATCAAGAGTGCCACCGTCTCAG 1080
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QY 1141 CGGTGCTCTCAGTAGGGGACTCGTTTCTTAGTGGTCAATCCAGGTATGCAAGTCAAT 1200
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QY 1021 ACCCCACAGATCAGCATGCTTTTCTCACCGACTACATCAAGAGTGCACCGGTCTCAG 1080
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QY 1081 TAATATTCTCTCGACAAAGAGCGCGGCGAGTATGCGATGCAAAACAGTGGGTG 1140
Db 1008 TAATATTCTCTCGACAAAGAGCGCGGCGAGTATGCGATGCAAAACAGTGGGTG 1057
QY 1141 CGGTGCTCTCTCAGGTAGGGGACTCGTTTCTTAGTGCTCATTCGAGGTATGCGATCGATT 1200
Db 1058 -----CAGGTATGCGATCGATT 1074
QY 1201 TGCCATGCCATGTCNAAGGAACCTTGTTCCAGGCTCAGTGCACCTCAACACCCCGTGGCT 1260
Db 1075 TGCCATGCCATGTCNAAGGAACCTTGTTCCAGGCTCAGTGCACCTCAACACCCCGTGGCT 1134
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Db 1195 AGCAAAAAGGTGGTGGTTCGTTACCGACAACCTGTATCCACCTTGACATTTTCACCA 1254
QY 1381 CCTCTTCCGCGGAGAACAGCATTTGGCGGAATACTATCCTCGGCTACTATAGCAAG 1440
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Db 1315 ATAGTCTTCTGATGGGACAACCGGTGGTGGCGGACAGGCTTCTGGGCGTCTCCAA 1374
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Db 1615 GCTCCGAGCGCGCTATGGGCTGAACCATCTCATCACTGGTTCGGCGCTCAGAACG 1674
QY 1801 CGGTTCAAGTGTGTTTCATTTCTTGGAAAGGAGCGTCTTTAGTTTGGAAAGGTTATATG 1860
Db 1675 CGGTTCAAGTGTGTTTCATTTCTTGGAAAGGAGCGTCTTTAGTTTGGAAAGGTTATATG 1734
QY 1861 GAAGGGCCATACGATCGGGTCAACGAGTGTGTCAGAAAGTGTGGCTAGGCTGGTGCCA 1920
Db 1735 GAAGGGCCATACGATCGGGTCAACGAGTGTGTCAGAAAGTGTGGCTAGGCTGGTGCCA 1794
QY 1921 GCAGCATAG 1929
Db 1795 GCAGCATAG 1803

RESULT 8
AR145484 1803 bp DNA linear PAT 08-AUG-2001
LOCUS Sequence 22 from patent US 6211435.
DEFINITION

ACCESSION AR145484
VERSION AR145484.1 GI:15107351
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1803)
AUTHORS Duvick J.P., Gilliam J.T., Maddox J.R., Crasta O.R. and Folkerts O.
TITLE Amino polyol amine oxidase polynucleotides and related polypeptides
and methods of use
JOURNAL Patent: US 6211435-A 22 03-APR-2001;
FEATURES Location/Qualifiers
 1..1803
 /organism="unknown"
BASE COUNT 424 a 501 c 502 g 376 t
ORIGIN

Query Match 83.1%; Score 1602.6; DB 6; Length 1803;
Best Local Similarity 91.7%; Pred. No. 0;
Matches 1769; Conservative 0; Mismatches 34; Indels 126; Gaps 2;

QY 1 ATGGCACTTGCACGAGCTACATCAATCCCCAAACGTCGCTCCCGACGAGGTATTCC 60
Db 1 ATGGCACTTGCACGAGCTACATCAATCCCCAAACGTCGCTCCCGACGAGGTATTCT 60
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Db 61 CACGTGGCGTAGGCCAGGAGGAGGAGTATGTGACAATAGCTGGACAGATTGGACAA 120
QY 121 GAGCTTTGGCGGTGACAGACCCAGCCTAGGAGAAACAGGTTGCCCAAGCATTCGCCAAT 180
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QY 181 CTGGAGCTTGCCTGCTGCGATTGGAGGCTCTTCAAGAGCTCACCAAGCTCAATTAC 240
Db 181 CTGGAGCTTGCCTGCTGCGATTGGAGGCTCTTCAAGAGCTCACCAAGCTCAATTAC 240
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QY 301 TTTGCCCTTGACAGGTCCTCTCTTGACGCTGGTGCAGTACCGGCTTGGCTTTCACCT 360
Db 301 TTTGCCCTTGACAGGTCCTCTCTTGACGCTGGTGCAGTACCGGCTTGGCTTTCACCT 360
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Db 361 GAATACCTCTTTGAGGTTGATGCCAGGCGCTGTCGAGGACACTCGACCCAGACAAAC 420
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QY 481 CAGCGCCCGGTCTGTCTGCTGCTGCTTTTGGAGCGATGATCGTGTAGGGGAAAGACT 540
Db 481 CAGCGCCCGGTCTGTCTGCTGCTGCTTTTGGAGCGATGATCGTGTAGGGGAAAGACT 540
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QY 721 CCTATGCTGACTCCCGGTTAAGCACAATCCACTTTGTGATGAGACCTCTGTCGAGTGT 780
Db 721 CCTATGCTGACTC----- 734

QY 781 AGAATACAGTCACTGACTCCACTTCCTCCAGCTGAGCGAGGAGTTGCAAGTGCACCTTCG 840
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QY 841 GGAACCTCTCCCGTATGGTCTCAGCTGATCGAAGAGTATAGCCTTGAAGACCCCAAGGC 900
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Db 888 AAATTCGCTGCTGTCTCAGCGTGGCAAAACACAGATCACACGCGCTCTCTCGGTGTGGA 947
QY 1021 AGCCACGAGATCAGATGCTTTTCTCACCAGTACATCAAGAGTGCACCGGTCTCAG 1080
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QY 1081 TAATATTGTCTCGGACAAGAAAGACGGCGGAGTATATCGGATGCAAAACAGGTGCGTG 1140
Db 1008 TANTATTCTCGGACAAGAAAGACGGCGGAGTATATCGGATGCAAAA----- 1057
QY 1141 CGGTGCTCTCAGTAGGGGACTCGTTTCTTAGTGGTCAATTCAGGTATGAGTCGATT 1200
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QY 1201 TGGCATGCCATGTCAAGGAACCTTGTTCAGGCTCAGTGCACCTCAACACCCCGCTCGT 1260
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QY 1261 GGAATTGAGCAGTCGGCGTCCGGCTGTATGATACGATCGGCTCGGGCGCGTGTCCGA 1320
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Db 1255 CTTCTTCCCGCCGAGAAAGCAAGCATTTGGCGGAAATCTATCTCGGCTACTATAGCAAG 1314
QY 1441 ATAGTCTTCGTATGGACAAACCCGTGGTGGCGCGCAACAGGCTTCTCGGGCGTCCCTCAA 1500
Db 1315 ATAGTCTTCGTATGGACAAACCCGTGGTGGCGCGCAACAGGCTTCTCGGGCGTCCCTCAA 1374
QY 1501 TCGAGCTGTACCCCATCTCATTTGCCAGATACCGAGTCCGAAGTCCGCAATGG 1560
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QY 1561 TCCATTACCTGTTTCATGTCGAGACCCGGGACCGGAAGTGGTCCCAAGTCCCAAGCAG 1620
Db 1435 TCCATTACCTGTTTCATGTCGAGACCCGGGACCGGAAGTGGTCCCAAGTCCCAAGCAG 1494
QY 1621 GTACGACAAAAGTCTGTCTGGGACCAACTCCCGCGAGCTACGAGAACCCGGGGCCCAA 1680
Db 1495 GTACGACAAAAGTCTGTCTGGGACCAACTCCCGCGAGCTACGAGAACCCGGGGCCCAA 1554
QY 1681 GTCCAGAGCCGGCCCAAGCTGCTCGAATCGAGTGGTCCGAGCAGCAGTATTTCAAAGA 1740
Db 1555 GTCCAGAGCCGGCCCAAGCTGCTCGAATCGAGTGGTCCGAGCAGCAGTATTTCAAAGA 1614
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QY 1801 CCGTTCAAGTGTGTTTCATTTTGGACGAGAGCGTCTTTAGTTTGGAAAGGTTATATG 1860
Db 1675 CCGTTCAAGAGTGTGTTTCATTTTGGACGAGAGCGTCTTTAGTTTGGAAAGGTTATATG 1734
QY 1861 GAAGGGGCCATACGATCGSGGTCAACAGGTGCTGCAGAGATTGTGGCTAGCCTGGTGCCA 1920

Db 1735 GAAGGGCCATCAGATCGSGTCAAGAGGTGCTCGAAGTGTGTGGCTAGCTGGTGCCA 1794
QY 1921 GCAGCATAG 1929
Db 1795 GCAGCATAG 1803
RESULT 9
ARI45462
LOCUS ARI45462 2490 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 32 from patent US 6211434.
ACCESSION ARI45462
VERSION ARI45462.1 GI:15107329
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2490)
AUTHORS Duvick, J.P., Gilliam, J.T. and Maddox, J.R.
TITLE Amino polyol amine oxidase polynucleotides and related polypeptides
JOURNAL and methods of use
FEATURES Location/Qualifiers
1. 2490
BASE COUNT 625 a 623 c 653 g 589 t
ORIGIN
Query Match 82.7%; Score 1596.2; DB 6; Length 2490;
Best Local Similarity 91.5%; Pred. No. 0;
Matches 1765; Conservative 0; Mismatches 38; Indels 126; Gaps 2;
QY 1 ATGGCACTTGCACGAGGTACATCAATCCCCAAACCGCTCCCGCAGGAGGTATTC 60
Db 688 ATGGCACTTGCACGAGGTACATCAATCCCCAAACCGCTCCCGCAGGAGGTATTC 747
QY 61 CACATCGGCGTAGGCGCAACGAAGCGAGGTATGTGACAATAGTGTGACAGATTGGACAA 130
Db 748 CACGTCGGCGTAGGCGCCAGAGGAGGAGGTATGTGACATAGCTGGACAGATTGGACAA 807
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Db 868 CTGAGAGCTTCGCTTGTGAGTTGGAGCCACTTCAACACGAGTCAACAGCTCAATTAC 927
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Db 988 TTTGCCCTTGACAGGCTCCCTCTTGGACAGTGGTGCACCTACCGGCTTGGCTTCACCT 1047
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Db 1048 GAATACCTCTTTGAGGTTGATGCCACGGCGCTGTCGCGGAGACAGACCCCGACAGAAC 1107
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Qy 601 AATGACAGCAACCAAGCGAAGTATCCAGATTGTTTGAAGAGATTTCAATTTGGAGGGGAG 660
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Qy 781 AGAATACAGTCACTGACTCCACTTCGTCAGCTGAGCGAGGAGTTCGAAGTGCATTGC 840
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Qy 1381 CCTCTTCCGCGGAGAACAGCATTTGGCGGAAATCTATCCTCGGCTACTATAGCAAG 1440
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Db 2422 GAAGGGCCATACGATCGGGTCAACGAGTGTGAGAGTTGTGGCTAGCCTGTGCGCA 2481
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AR145489
LOCUS AR145489 2490 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 32 from patent US 6211435.
ACCESSION AR145489
VERSION AR145489.1 GI:15107356
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2490)
AUTHORS Duvick,J.P., Gilliam,J.T., Maddox,J.R., Crasta,O.R. and Folkerts,O.
TITLE Amino polyol amine oxidase polynucleotides and related polypeptides
and methods of use
JOURNAL Patent: US 6211435-A 32 03-APR-2001;
FEATURES
source Location/Qualifiers
BASE COUNT 625 a 623 c 653 g 589 t
ORIGIN
Query Match 82.7%; Score 1596.2; DB 6; Length 2490;
Best Local Similarity 91.5%; Pred. No. 0;
Matches 1765; Conservative 0; Mismatches 38; Indels 126; Gaps 2;
Qy 1 ATGGCACTTGCACCGAGCTACATCAATCCCAAGCTGCGCTCCCAAGCAGGATTTCC 60
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Db 868 CTGCGAGCTTGGCTTGTGTCAGTTGGAGCTCTTCAAACGACGTCAACAGCTCAATTAC 927
Qy 241 TACATCGTCACTACGCCCGAGCAAACTCACGCCAATTGGAGATGGGTGAAGTCTACC 300
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Db 988 TTTGCCCTTGACAGGCTCCCTCTTGCACCGTGGTCCAGTGTGCGCTTGTCTTCACT 1047
Qy 361 GAATACCTCTTTGAGGTTGATGCCACGGCGCTGGTGCAGGACACTCGACCCCGAGACAAC 420
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QY 895 CAAGCGAGCCCTCAGGCGAAGCGGCTCGACAGTGTGAGCTTCGGCGCACTACTGTGAGAA 954
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RESULT 13
LOCUS AR145459 2976 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 26 from patent US 6211434.
ACCESSION AR145459
VERSION AR145459.1 GI:15107326
KEYWORDS .
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2976)
AUTHORS Duvick,J.P., Gilliam,J.T. and Maddox,J.R.
TITLE Amino polyol amine oxide polynucleotides and related polypeptides
and methods of use
JOURNAL Patent: US 6211434-A 26 03-APR-2001;
FEATURES
source Location/Qualifiers
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/organism="unknown"
BASE COUNT 564 a 932 c 926 g 554 t
ORIGIN
Query Match 62.8%; Score 1212.2; DB 6; Length 2976;
Best Local Similarity 90.2%; Pred. No. 1.4e-313;
Matches 1372; Conservative 0; Mismatches 23; Indels 126; Gaps 2;
QY 409 ACCCCAGACAACGTTGCGGACGTGTGTAGTGTGGCGCTGGCTTGGAGCAGC 468
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| Qy | 1129 | AACAGGTGCGTGCCTCTCAGGTAGGGACTCGTTTCTTAGTGTCTATTCAGGT | 1188 |
| Db | 2229 | AA-----CAGGT | 2235 |
| Qy | 1189 | ATGCAGTCGATTTGCCATGCCATGTCAAAGAACTTGTTCAGGCTCAGTGCACCTCAAC | 1248 |
| Db | 2236 | ATGCAGTCGATTTGCCATGCCATGTCAAAGAACTTGTTCAGGCTCAGTGCACCTCAAC | 2295 |
| Qy | 1249 | ACCCCGTGCCTGGAATTGAGCAGTCGCGCTCGCGCTGTATAGTATGATCGGCTCGGGC | 1308 |
| Db | 2296 | ACCCCGTGCCTGGAATTGAGCAGTCGCGCTCGCGCTGTATAGTATGATCGGCTCGGGC | 2355 |
| Qy | 1309 | GCGGTGTCGGAAGCAAAAAGTGGTTCGTTACCGACAACTGTATCCACCTTG | 1368 |
| Db | 2356 | GCGGTGTCGGAAGCAAAAAGTGGTTCGTTACCGACAACTGTATCCACCTTG | 2415 |
| Qy | 1369 | ACATTTTCCACACCTCTTCGCGCGGAGCAAGACATTCGCGGAAATATCTCTCGG | 1428 |
| Db | 2416 | ACATTTTCCACACCTCTTCGCGCGGAGCAAGACATTCGCGGAAATATCTCTCGG | 2475 |
| Qy | 1429 | TACTATAGCAAGTAGTCTTCGTATGGCAACCCGTTGGCGGCAACAGGCTTCTCG | 1488 |
| Db | 2476 | TACTATAGCAAGTAGTCTTCGTATGGCAACCCGTTGGCGGCAACAGGCTTCTCG | 2535 |
| Qy | 1489 | GCGTCTCTCCAAATCGAGCTGTGACCCCATCTCATTTGCCAGAGATACCAAGTCGAAGTC | 1548 |
| Db | 2536 | GCGTCTCTCCAAATCGAGCTGTGACCCCATCTCATTTGCCAGAGATACCAAGTCGAAGTC | 2595 |
| Qy | 1549 | GATCGGCATGGTCCATTACCTGTTTCATGTCGGAGACCCGGGACGGAAGTGTCCAA | 1608 |
| Db | 2596 | GATCGGCATGGTCCATTACCTGTTTCATGTCGGAGACCCGGGACGGAAGTGTCCAA | 2655 |
| Qy | 1609 | CAGTCCAAGCAGGTACGACAAAGTCTCTGCGGACCAACTCCGCGAGCTCAGGAAAC | 1668 |
| Db | 2656 | CAGTCCAAGCAGGTACGACAAAGTCTCTGCGGACCAACTCCGCGAGCTCAGGAAAC | 2715 |
| Qy | 1669 | GCGGGGCCCAAGTCCAGAGCCGCGCAACGTGCTCGAAATCGAGTGGTCCGAAGCAGCAG | 1728 |
| Db | 2716 | GCGGGGCCCAAGTCCAGAGCCGCGCAACGTGCTCGAAATCGAGTGGTCCGAAGCAGCAG | 2775 |
| Qy | 1729 | TATTTCCAAGAGCTCCGAGCGCGCTATGGGCTGAACGATCTCATCAGCTGGGTCG | 1788 |
| Db | 2776 | TATTTCCAAGAGCTCCGAGCGCGCTATGGGCTGAACGATCTCATCAGCTGGGTCG | 2835 |
| Qy | 1789 | GCGCTCAGAACCGCGTTCAAGTGTTCATTTCTGGAACGGAGAGCTCTTTAGTTGG | 1848 |
| Db | 2836 | GCGCTCAGAACCGCGTTCAAGTGTTCATTTCTGGAACGGAGAGCTCTTTAGTTGG | 2895 |
| Qy | 1849 | AAAGGTTATATGGAAGGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAAGTTGGCT | 1908 |
| Db | 2896 | AAAGGTTATATGGAAGGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAAGTTGGCT | 2955 |
| Qy | 1909 | AGCCTGGTCCAGCAGCATAG | 1929 |
| Db | 2956 | AGCCTGGTCCAGCAGCATAG | 2976 |
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| LOCUS | AR145486 | 2976 bp | DNA linear PAT 08-AUG-2001 |
| DEFINITION | AR145486 | Sequence 26 from patent US 6211435. | |
| ACCESSION | AR145486 | | |
| VERSION | AR145486.1 | GI:15107353 | |
| KEYWORDS | | | |
| SOURCE | Unknown. | | |
| ORGANISM | Unknown. | | |
| REFERENCE | 1 (bases 1 to 2976) | | |
| AUTHORS | Duvick,J.P., Gilliam,J.T., Maddox,J.R., Crasta,O.R. and Folkerts,O. | | |
| TITLE | Amino polyol amine oxidase polynucleotides and related polypeptides and methods of use | | |
| JOURNAL | Patent: US 6211435-A 26 03-APR-2001; | | |
| FEATURES | Location/Qualifiers | | |

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| | Matches 1372; Conservative | 0; Mismatches 23; Indels 126; Gaps 2; | |
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| Db | 1582 | AGCAAGAACAGTTTCGGACGCTGTAGTGTGGCGCTGGCTTGGAGCGTTTGAGACG | 1641 |
| Qy | 469 | GCACGCAAAAGTCCAGCGCCCGCTGTCTCTCGCTCGTTTCTTAGGCGATGATCGTGA | 528 |
| Db | 1642 | GCACGCAAAAGTCCAGCGCCCGCTGTCTCTCGCTCGTTTCTTAGGCGATGATCGTGA | 1701 |
| Qy | 529 | GGGGAAAGACTCTGAGCGTACAATCGGTCGCCGACGACGACTATCAAGACCTCGC | 588 |
| Db | 1702 | GGGGAAAGACTCTGAGCGTACAATCGGTCGCCGACGACGACTATCAAGACCTCGC | 1761 |
| Qy | 589 | GCTGCGTGATCAATCAGACGACCAACCAAGATTCAGATTCTTTGAAAGATTTTCA | 648 |
| Db | 1762 | GCTGCGTGATCAATCAGACGACCAACCAAGATTCAGATTCTTTGAAAGATTTTCA | 1821 |
| Qy | 649 | TTGGAGGGCGAGTCCAGAGGACGACCGGAAATTCATTCATCAAGCAACAGCGGTACA | 708 |
| Db | 1822 | TTGGAGGGCGAGTCCAGAGGACGACTGGAATTCATTCATCAAGCAACAGCGGTACA | 1881 |
| Qy | 709 | ACACTACAGCTCCTTATGTTGACTCCCGGTAAAGCAATCCCACTTTGTGATGAGAC | 768 |
| Db | 1882 | ACCATTACAGCTCCTTATGTTGACTC-----CTTGCTGAGCGAGGAGTTGC | 1907 |
| Qy | 769 | TCGTGCGAGTAGAATACAGTCACTCCACTTCGTCAGCTGAGCGAGAGGTTGC | 828 |
| Db | 1908 | -----CTTGCTGAGCGAGGAGTTGC | 1928 |
| Qy | 829 | AAGTGCACTTGGGAACTCCTCCCGTATGCTCTCAGCTGATCGAAGATATAGCCTTGA | 888 |
| Db | 1929 | AAGTGCACTTGGGAACTCCTCCCGTATGCTCTCAGCTGATCGAAGATATAGCCTTGA | 1988 |
| Qy | 889 | AGACCCAGGGAGCGCTCAGCGAAGCGCTGCACAGTGTGAGCTTCGCCCACTACTG | 948 |
| Db | 1989 | AGACCTTCAAGGGAGCGCTCAGCGAAGCGCTGCACAGTGTGAGCTTCGCCCACTACTG | 2048 |
| Qy | 949 | TGAGAAGGACCTAAACTTCCTGCTTCTCAGCGTGGCAACACAGATCACACGCGCTC | 1008 |
| Db | 2049 | TGAGAAGGACCTAAACTTCCTGCTTCTCAGCGTGGCAACACAGATCACACGCGCTC | 2108 |
| Qy | 1009 | GCTCGGTGGAAGCCACGAGATCAGCATGCTTTTTCACCGACTACATCAAGAGTGC | 1068 |
| Db | 2109 | GCTCGGTGGAAGCCACGAGATCAGCATGCTTTTTCACCGACTACATCAAGAGTGC | 2168 |
| Qy | 1069 | CACCGTCTCAGTAATATTGCTCGGACAAGAAAGCGGGGCGAGTATCGGATGCAA | 1128 |
| Db | 2169 | CACCGTCTCAGTAATATTGCTCGGACAAGAAAGCGGGGCGAGTATCGGATGCAA | 2228 |
| Qy | 1129 | AACAGTGCCTGCGGTCTCCTCTCAGGTAGGGACTCGTTTCTTAGTGTCTATTCAGGT | 1188 |
| Db | 2229 | AA-----CAGGT | 2235 |
| Qy | 1189 | ATGCAGTCGATTTGCCATGCCATGTCAAAGAACTTGTTCAGGCTCAGTGCACCTCAAC | 1248 |
| Db | 2236 | ATGCAGTCGATTTGCCATGCCATGTCAAAGAACTTGTTCAGGCTCAGTGCACCTCAAC | 2295 |
| Qy | 1249 | ACCCCGTGCCTGGAATTGAGCAGTCGCGCTCGCGCTGTATAGTATGATCGGCTCGGGC | 1308 |
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| Qy | 1309 | GCGGTGTCGGAAGCAAAAAGTGGTTCGTTACCGACAACTGTATCCACCTTG | 1368 |
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| Qy | 1369 | ACATTTTCAACACCTCTTCCGCGCAGAGCAAGATTTGGCGGAAAAATCATCTCTCGG | 1428 |
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| Qy | 1429 | TACTATAGCAAGATAGTCTTTCGTATGGGACAAACCCGTGTGGCGGAAACAAAGCTTCTCG | 1488 |
| Db | 2476 | TACTATAGCAAGATAGTCTTTCGTATGGGACAAACCCGTGTGGCGGAAACAAAGCTTCTCG | 2535 |
| Qy | 1489 | GGCGTCTCCAATCGAGCTGTGACCCCATCTCATTTGCCAGAGATACCGAGCATCGAAGTC | 1548 |
| Db | 2536 | GGCGTCTCCAATCGAGCTGTGACCCCATCTCATTTGCCAGAGATACCGAGCATCGAAGTC | 2595 |
| Qy | 1549 | GATCGCAATGGTCCATTACCTGTTTCATGGTCGGAGACCCGGACGGAAGTGGTCCCAA | 1608 |
| Db | 2596 | GATCGCAATGGTCCATTACCTGTTTCATGGTCGGAGACCCGGACGGAAGTGGTCCCAA | 2655 |
| Qy | 1609 | CAGTCCAGCAGGTACGACAAAAGTCTGTCTGGACCAACTCCGCGCAGCCTACGAGAAC | 1668 |
| Db | 2656 | CAGTCCAGCAGGTACGACAAAAGTCTGTCTGGACCAACTCCGCGCAGCCTACGAGAAC | 2715 |
| Qy | 1669 | GCCGGGCCCCAAGTCCGAGAGCGGCCAACGTCTCGAAATCGAGTGGTCGAAGCAGCAG | 1728 |
| Db | 2716 | GCCGGGCCCCAAGTCCGAGAGCGGCCAACGTCTCGAAATCGAGTGGTCGAAGCAGCAG | 2775 |
| Qy | 1729 | TATTTCCAAAGAGCTCCGAGCGCGCTATGGGCTGAACGATCTCATCACACTGGGTTGG | 1788 |
| Db | 2776 | TATTTCCAAAGAGCTCCGAGCGCGCTATGGGCTGAACGATCTCATCACACTGGGTTGG | 2835 |
| Qy | 1789 | GCCTCAGAACCGGTTCAAGTGTGTTCATTCGTTGGACGGAGACGTCCTTAGTTGG | 1848 |
| Db | 2836 | GCCTCAGAACCGGTTCAAGTGTGTTCATTCGTTGGACGGAGACGTCCTTAGTTGG | 2895 |
| Qy | 1849 | AAAGGGTATATGAAGGGGCCATFACGATCGGGTCAACAGAGTGCTGCAGAAATTGTGGCT | 1908 |
| Db | 2896 | AAAGGGTATATGAAGGGGCCATFACGATCGGGTCAACAGAGTGCTGCAGAAATTGTGGCT | 2955 |
| Qy | 1909 | AGCCTGGTCCACGACATAG | 1929 |
| Db | 2956 | AGCCTGGTCCACGACATAG | 2976 |
| RESULT 15 | | | |
| AR145458 | | | |
| LOCUS | | | |
| DEFINITION | | | |
| ACCESSION | | | |
| VERSION | | | |
| KEYWORDS | | | |
| SOURCE | | | |
| ORGANISM | | | |
| REFERENCE | | | |
| AUTHORS | | | |
| TITLE | | | |
| JOURNAL | | | |
| FEATURES | | | |
| BASE COUNT | | | |
| ORIGIN | | | |
| Query Match | | | |
| Best Local Similarity | | | |
| Matches 1372; Conservative | | | |
| Qy | 409 | ACCCACAGAACAGTTCCGACGTGTAGTGGCGGTGGCTTGGCTTGGAGACG | 468 |
| Db | 1609 | AGCAAGAACAGTTCCGACGTGTAGTGGCGGTGGCTTGGCTTGGAGACG | 1668 |
| Qy | 469 | GCACGAAAGTCCAGGCCCGCGGTCTGTCTCCCTCGTTCCTTGGCGCATGATCGTGTA | 528 |
| Db | 1669 | GCACGAAAGTCCAGGCCCGCGGTCTGTCTCCCTCGTTCCTTGGCGCATGATCGTGTA | 1728 |

| | | | |
|----|------|---|------|
| Qy | 529 | GGGGGAAAGACTCTGAGCGTACAATFCGGGTCCGCGCAGGAGCACTATCAACGACCTCGGC | 588 |
| Db | 1729 | GGGGGAAAGACTCTGAGCGTACAATFCGGGTCCGCGCAGGAGCACTATCAACGACCTCGGC | 1788 |
| Qy | 589 | GCTGCGTGGATCAATGACAGCAACCAAGCGAAGTATCCACATGTTTGAAGATTTTCAT | 648 |
| Db | 1789 | GCTGCGTGGATCAATGACAGCAACCAAGCGAAGTATCCACATGTTTGAAGATTTTCAT | 1848 |
| Qy | 649 | TTGAGGCGGAGCTCCAGAGGACGACCGGAAATTCATATCCATCAAGCACAAAGCGGTACA | 708 |
| Db | 1849 | TTGAGGCGGAGCTCCAGAGGACGACGCGAAATTCATATCCATCAAGCACAAAGCGGTACA | 1908 |
| Qy | 709 | ACCACTACAGCTCCTTATGTGTGATCCGCCGTAAGACAATCCCACTTTGTGTGATGAGAC | 768 |
| Db | 1909 | ACCACTACAGCTCCTTATGTGTGATCCGCCGTAAGACAATCCCACTTTGTGTGATGAGAC | 1934 |
| Qy | 769 | TCTGTGAGTGTAGAATACAGTCACTGACTCCACTTCGTCCAGCTGAGCGAGGAGTTGC | 828 |
| Db | 1935 | -----CTTGTGAGCGAGGAGTTGC | 1955 |
| Qy | 829 | AAGTCACTTCGGAACTCTCCCGGTATGTCTCAGCTGATCGAAGAGTATAGCCTTGA | 888 |
| Db | 1956 | AAGTCACTTCGGAACTCTCCCGGTATGTCTCAGCTGATCGAAGAGTATAGCCTTGA | 2015 |
| Qy | 889 | AGACCCCAAGCGGAGCCCTCAGCGCAAGCGCTCGACAGTGTGAGCTTCGGCGCACTACTG | 948 |
| Db | 2016 | AGACCTCAAGCGGAGCCCTCAGCGCAAGCGCTCGACAGTGTGAGCTTCGGCGCACTACTG | 2075 |
| Qy | 949 | TGAGAAGGACCTAACTTGGCTGTCTCAGCGTGCAGCAACCAAGAGTATCACACGCGTCT | 1008 |
| Db | 2076 | TGAGAAGGAACTAACTTGGCTGTCTCAGCGTGCAGCAACCAAGAGTATCACACGCGTCT | 2135 |
| Qy | 1009 | GCTCGTGTGAAGCCACGAGATCAGATGCTTTTCTCACCGACTACATCAAGAGTGC | 1068 |
| Db | 2136 | GCTCGTGTGAAGCCACGAGATCAGATGCTTTTCTCACCGACTACATCAAGAGTGC | 2195 |
| Qy | 1069 | CACCGTCTCAGTAATATTGTCGACAGAAAGAGCGGCGAGTATATGCGATGCA | 1128 |
| Db | 2196 | CACCGTCTCAGTAATATTGTCGAGACAGAAAGAGCGGCGAGTATATGCGATGCA | 2255 |
| Qy | 1129 | AACAGGTGCGTGCCTCTCAGGTAGGGACTCGTTTCTTAGTGGTCAATCCAGGT | 1188 |
| Db | 2256 | AA-----CAGGT | 2262 |
| Qy | 1189 | ATGAGTGCATTTGCCATGCCATGTCAAAGAACTTGTTCAGGCTCAGTGCACCTCAAC | 1248 |
| Db | 2263 | ATGAGTGCATTTGCCATGCCATGTCAAAGAACTTGTTCAGGCTCAGTGCACCTCAAC | 2322 |
| Qy | 1249 | ACCCCGTTCGCTGGAATGAGCAGTCCGCGTGTATAGTACGATCGGCTCGGGC | 1308 |
| Db | 2323 | ACCCCGTTCGCTGGAATGAGCAGTCCGCGTGTACGATCGGCTCGGGC | 2382 |
| Qy | 1309 | GCGGTTCGGAAGCAAAAAGTGGTGGTTTCCGTACCGACAACTTGTATCCCACTTG | 1368 |
| Db | 2383 | GCGGTTCGGAAGCAAAAAGTGGTGGTTTCCGTACCGACAACTTGTATCCCACTTG | 2442 |
| Qy | 1369 | ACATTTTCACCACTCTTCCCGCGAGAAAGCAGCATTTGGCGGAAAATCTATCTCGGC | 1428 |
| Db | 2443 | ACATTTTCACCACTCTTCCCGCGAGAAAGCAGCATTTGGCGGAAAATCTATCTCGGC | 2502 |
| Qy | 1429 | TACTATAGCAAGATAGTCTTTCGTATGGCAACCCCGTGGTGGCGGAAAGCTTCTCG | 1488 |
| Db | 2503 | TACTATAGCAAGATAGTCTTTCGTATGGCAACCCCGTGGTGGCGGAAAGCTTCTCG | 2562 |
| Qy | 1489 | GGGTCTCTCAATGAGCTGTGACCCCATCTCATTTGCCAGAGATACCGAGCATCGAAGTC | 1548 |
| Db | 2563 | GGGTCTCTCAATGAGCTGTGACCCCATCTCATTTGCCAGAGATACCGAGCATCGAAGTC | 2622 |
| Qy | 1549 | GATCGCAATGGTCCATTTACCTGTTTCATGTCGGAGACCCGGAGCGGAGTGGTCCCAA | 1608 |
| Db | 2623 | GATCGCAATGGTCCATTTACCTGTTTCATGTCGGAGACCCGGAGCGGAGTGGTCCCAA | 2682 |

| | | | |
|----|------|--|------|
| QY | 1609 | CAGTCCAAGCAGGTACGACAAAGTCTGTCTGGGACCAACTCCGGCGAGCCTACGAGAAC | 1668 |
| Db | 2683 | | |
| QY | 1669 | GCGGGGCCCAAGTCCAGAGCCGGCCAACTGCTCGAAATCGAGTGTCTGAAAGCAGCAG | 1728 |
| Db | 2743 | | |
| QY | 1729 | TATTTCCAAAGGAGTCCGAGCGCGTCTATGGGCTGAACGATCTCATCACACTGGGTTCTG | 1788 |
| Db | 2803 | | |
| QY | 1789 | GCGCTCAGAACCCCGTTCAAGTGTCTTCATTTCTGGAACGGAGACGCTCTTTAGTTTGG | 1848 |
| Db | 2863 | | |
| QY | 1849 | AAAGGTATATGGAAGGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAGTTGTGGCT | 1908 |
| Db | 2923 | | |
| QY | 1909 | AGCCTGGTGCCAGCAGCATAG | 1929 |
| Db | 2983 | | |

Search completed: November 12, 2002, 04:43:39
Job time : 5111 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 12, 2002, 02:14:19 ; Search time 416 Seconds
(without alignments)
10442.560 Million cell updates/sec

Title: US-09-771-045A-35
Perfect score: 1929
Sequence: 1 atggcaactgaccagagcta.....gccttggtgccagcagcatag 1929

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues
Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | ID | Description |
|------------|--------|---------------|--------|----|------------------------------|
| 1 | 1929 | 100.0 | 1929 | 21 | AAZ58382 Exophiala spinifer |
| 2 | 1925.8 | 99.8 | 1929 | 21 | AAZ58383 Exophiala spinifer |
| 3 | 1851.4 | 96.0 | 1930 | 21 | AAZ58384 Exophiala spinifer |
| 4 | 1792.2 | 92.9 | 1928 | 21 | AAZ58386 Rhinocladiaella atr |
| 5 | 1789 | 92.7 | 1928 | 21 | AAZ58387 Rhinocladiaella atr |
| 6 | 1787.4 | 92.7 | 1928 | 21 | AAZ58385 Rhinocladiaella atr |
| 7 | 1602.6 | 83.1 | 1803 | 21 | AAZ58402 Exophiala spinifer |
| 8 | 1602.6 | 83.1 | 1803 | 21 | AAZ60641 DNA encoding a ful |
| 9 | 1596.2 | 82.7 | 2490 | 21 | AAZ58407 DNA encoding GST-t |

| | | | | | |
|----|--------|------|-------|----|-----------------------------|
| 10 | 1596.2 | 82.7 | 2490 | 21 | AAZ60646 DNA encoding a fus |
| 11 | 1319 | 68.4 | 1442 | 21 | AAZ58393 Amino polyol amine |
| 12 | 1319 | 68.4 | 1442 | 21 | AAZ60631 DNA encoding an am |
| 13 | 1212.2 | 62.8 | 2976 | 21 | AAZ58404 DNA encoding funon |
| 14 | 1212.2 | 62.8 | 2976 | 21 | AAZ60643 DNA encoding a fus |
| 15 | 1212.2 | 62.8 | 3003 | 21 | AAZ58403 DNA encoding funon |
| 16 | 1212.2 | 62.8 | 3003 | 21 | AAZ60642 DNA encoding a fus |
| 17 | 1212.2 | 62.8 | 3591 | 21 | AAZ58406 DNA encoding funon |
| 18 | 1212.2 | 62.8 | 3591 | 21 | AAZ60645 DNA encoding a fus |
| 19 | 1212.2 | 62.8 | 3618 | 21 | AAZ58405 DNA encoding funon |
| 20 | 1212.2 | 62.8 | 3618 | 21 | AAZ60644 DNA encoding a fus |
| 21 | 1212 | 62.8 | 1392 | 21 | AAZ58394 Amino polyol amine |
| 22 | 1212 | 62.8 | 1392 | 21 | AAZ60633 DNA encoding an am |
| 23 | 1212 | 62.8 | 1464 | 21 | AAZ58401 DNA encoding amino |
| 24 | 1212 | 62.8 | 1464 | 21 | AAZ60640 DNA encoding an am |
| 25 | 1212 | 62.8 | 1673 | 21 | AAZ58395 Amino polyol amine |
| 26 | 1212 | 62.8 | 1673 | 21 | AAZ60638 DNA encoding an am |
| 27 | 1212 | 62.8 | 2079 | 21 | AAZ58400 DNA encoding GST-t |
| 28 | 1212 | 62.8 | 2079 | 21 | AAZ60639 DNA encoding an am |
| 29 | 1211 | 62.8 | 1389 | 21 | AAZ58392 Amino polyol amine |
| 30 | 1211 | 62.8 | 1389 | 21 | AAZ60630 DNA encoding an am |
| 31 | 361.4 | 18.7 | 372 | 21 | AAZ58388 Exophiala spinifer |
| 32 | 361.4 | 18.7 | 372 | 21 | AAZ60654 Nucleotide sequenc |
| 33 | 174 | 9.0 | 182 | 21 | AAZ58389 Nucleotide sequenc |
| 34 | 174 | 9.0 | 182 | 21 | AAZ60663 Propionibacterium |
| 35 | 49.2 | 2.6 | 66788 | 23 | AAZ59515 Human monoamine ox |
| 36 | 40.8 | 2.1 | 1619 | 22 | AAZ62793 Gene #2392 used to |
| 37 | 40.8 | 2.1 | 2491 | 22 | AAZ62783 Lung cancer relate |
| 38 | 40.8 | 2.1 | 2491 | 24 | ABN95894 Kidney cancer rela |
| 39 | 40.8 | 2.1 | 2491 | 24 | ABL61827 Micrococcal putres |
| 40 | 40.8 | 2.1 | 2491 | 24 | ABL66273 Mycobacterium tube |
| 41 | 40.8 | 2.1 | 2491 | 24 | ABL68529 Drosophila melanog |
| 42 | 40.4 | 2.1 | 2386 | 15 | AAQ63477 Drosophila melanog |
| 43 | 40.2 | 2.1 | 1347 | 22 | AAC97010 |
| 44 | 39.4 | 2.0 | 3559 | 23 | ABL23641 |
| 45 | 39.4 | 2.0 | 3645 | 23 | ABL18747 |

ALIGNMENTS

RESULT 1
AAZ58382
ID AAZ58382 standard; DNA; 1929 BP.

XX AC AAZ58382;

XX DT 23-MAY-2000 (first entry)

XX DE Exophiala spinifera amino polyol amine oxidase ESP002_C2 DNA.

XX KW Amino polyol amine oxidase; fumonisin; mycotoxin; transgenic plant;

XX KX detoxification; animal feed; silage; selectable marker; ds.

XX OS Exophiala spinifera.

XX FH Key Location/Qualifiers

XX FT CDS 1..1929

XX FT /tag= a

XX FT /note= "contains introns"

XX FT Intron 739..811

XX FT /tag= b

XX FT Intron 1134..1186

XX FT /tag= c

XX WO200004159-A1.

XX PN 27-JAN-2000.

XX PD 08-JUL-1999;

XX PF 99WO-US15454.

XX PR 15-JUL-1998;

XX PR 98US-0092936.

XX PR 21-MAY-1999;

XX PR 99US-0135391.

Db 1561 TCCATTACCTGTTTCATGTCGGAGACCCGGGACGGAGTGGTCCCNACAGTCCAAGCAG 1620
Qy 1621 GTACGACAAAAGTCTGTCTGGGACCAACTCCGGCGACGCTTACGAGAACGCCGGGGCCCAA 1680
Db 1621 GTACGACAAAAGTCTGTCTGGGACCAACTCCGGCGACGCTTACGAGAACGCCGGGGCCCAA 1680
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Qy 1741 GCTCCGAGCGCGCTATGGGCTGAAGCATCTCATCACTGGGTTCCGGCGCTCAGAAGC 1800
Db 1741 GCTCCGAGCGCGCTATGGGCTGAAGCATCTCATCACTGGGTTCCGGCGCTCAGAAGC 1800
Qy 1801 CCGTTCAAGTGTGTTTCATTTGCTGGAACGAGACGCTTTAGTTTGGAAAGGATATG 1860
Db 1801 CCGTTCAAGTGTGTTTCATTTGCTGGAACGAGACGCTTTAGTTTGGAAAGGATATG 1860
Qy 1861 GAAGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAGTTGTGGCTAGCCTGGTGCCA 1920
Db 1861 GAAGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAGTTGTGGCTAGCCTGGTGCCA 1920
Qy 1921 GCAGCATAG 1929
Db 1921 GCAGCATAG 1929
RESULT 2
AAZ58383
ID AAZ58383 standard; DNA; 1929 BP.
XX AC AAZ58383;
XX DT 23-MAY-2000 (first entry)
XX DE Exophiala spinifera amino polyol amine oxidase ESP002_C3 DNA.
KW Amino polyol amine oxidase; funonisin; mycotoxin; transgenic plant;
KW detoxification; animal feed; silage; selectable marker; ds.
XX OS Exophiala spinifera.
FH key Location/Qualifiers
FH CDS 1..1929
FT /*tag= a
FT /*note= "contains introns"
FT intron 739..811
FT intron /*tag= b
FT intron 1134..1186
FT /*tag= c
XX WO200004159-A1.
PN 27-JAN-2000.
XX 08-JUL-1999; 99WO-US15454.
XX 15-JUL-1998; 98US-0092936.
XX 21-MAY-1999; 99US-0135391.
XX (PION-) PIONEER HI-BRED INT INC.
XX (CURA-) CURAGEN CORP.
XX Duwick JP, Gilliam JT, Maddox JR;
PI WPI; 2000-182425/16.
DR P-PSDB; AAZ58901.
XX New isolated polynucleotides, polypeptides useful for detecting and
PT degrading funonisin or structurally related mycotoxin in processed
PT grain or in silage -
XX

PS Claim 1; Page 139-140; 154pp; English.
XX The present sequence is that of an isolated nucleic acid,
CC designated ESP002_C3, of Exophiala spinifera isolate ESP002,
CC which encodes an amino polyol amine oxidase (APAO, see AAY58901),
CC capable of degrading funonisin, its hydrolysis product API, and
CC related mycotoxins. The DNA was obtained by PCR amplification of
CC ESP002 mycelial DNA using primers based on APAO of E. spinifera
CC ATCC 74269. The invention provides APAO polynucleotides (see
CC AAZ58383-87) and polypeptides (see AAY58900-05) of E. spinifera and
CC Rhinocladiella atrovirens. The polynucleotides are used to transform
CC plant cells normally susceptible to Fusarium or other toxin-producing
CC fungus infection. Transgenic plants can be regenerated from the
CC transformed plant cells. Also provided are methods for expressing
CC both APAO and a funonisin-esterase in a transgenic plant, and for
CC producing APAO enzyme in prokaryotic and non-plant eukaryotic
CC systems. Transgenic plants capable of degrading funonisin or of
CC producing the degrading enzymes are provided. Methods for
CC detoxification of grain, grain processing, silage, food crops and
CC in animal feed and rumen microorganisms are also disclosed. APAO
CC polynucleotide is also useful as a selectable marker.
XX Sequence 1929 BP; 451 A; 539 C; 532 G; 407 T; 0 other;
SQ Query Match 99.8%; Score 1925.8; DB 21; Length 1929;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1927; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Db 61 CACATCGGCTAGGCCCAAGGAGGATGTGTGACAAATAGCTGGACAGATTGGACAA 120
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Db 121 GACGCTTTGGGCGTGACAGACCCAGCTACGAGAAACAGGTTGCCCAAGCATTCGCAAT 180
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Db 181 CTGGGAGCTTGCCTTGGCTGAGTTGGAGCTCTTCAAGCAGCTCACCAGCTCAATTAC 240
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Db 361 GAATACCTTTGAGTTGATGCCAGGCGCTGGTCCAGGACACTCGACCCAGACAAC 420
Qy 421 GTTCCGAGCTGTGTGTGGCTGGCTTGGAGCGTTGGAGACGGCACCAAGTC 480
Db 421 GTTCCGAGCTGTGTGTGGCTGGCTTGGAGCGTTGGAGACGGCACCAAGTC 480
Qy 481 CAGCCCGCGGCTCTGCTCCCTCGCTTGTAGGCGGATGGATCGTGTAGGGGAAAGACT 540
Db 481 CAGCCCGCGGCTCTGCTCCCTCGCTTGTAGGCGGATGGATCGTGTAGGGGAAAGACT 540
Qy 541 CTGAGCGTACAATCGGGTCCCGGAGGACACTATCAACACCTCGCGCTGGTGATC 600
Db 541 CTGAGCGTACAATCGGGTCCCGGAGGACACTATCAACACCTCGCGCTGGTGATC 600
Qy 601 AATCAGACGACCAAAAGGAGTATCCAGATTTGTTTGAAGATTTTCAATTTGGAGGCGAG 660
Db 601 AATCAGACGACCAAAAGGAGTATCCAGATTTGTTTGAAGATTTTCAATTTGGAGGCGAG 660
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Db 661 CTCCAGAGGACGCGGAAATCAATCCATCAAGCACAACGCTACACGCT 720
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Db 721 CCTTATGGTGACTCCCGGTAAAGCACAAATCCACTTTGTGATCAGACCTCTGTCGAGTGT 780
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QY 1921 GCAGCATAG 1929
Db 1921 GCAGCATAG 1929
RESULT 3
AAZ58384
ID AAZ58384 standard; DNA; 1930 BP.
XX AAZ58384;
AC AAZ58384;
XX 23-MAY-2000 (first entry)
XX Exophiala spinifera amino polyol amine oxidase ESP003_C12 DNA.
DE Amino polyol amine oxidase; fumonisin; mycotoxin; transgenic plant;
KW detoxification; animal feed; silage; selectable marker; ds.
XX Exophiala spinifera.
OS
FH Key Location/Qualifiers
FT CDS 1..1930
FT /tag= a
FT /note= "contains introns"
FT intron 739..811
FT /tag= b
FT intron 1134..1187
FT /tag= c
XX WO200004159-A1.
PN
XX
PD 27-JAN-2000.
XX
XX 08-JUL-1999; 99WO-US15454.
XX
XX 15-JUL-1998; 98US-0092936.
PR 21-MAY-1999; 99US-0135391.
XX
XX (PION-) PIONEER HI-BRED INT INC.
PA (CURA-) CURAGEN CORP.
XX
XX DuVick JP, Gilliam JT, Maddox JR;
XX
XX WPI; 2000-182425/16.
DR P-PSDB; AAY58902.
XX
XX New isolated polynucleotides, polypeptides useful for detecting and
PT degrading fumonisin or structurally related mycotoxin in processed
PT grain or in silage
XX
PS Claim 1; Page 141-142; 154pp; English.
XX
CC The present sequence is that of an isolated nucleic acid,
CC designated ESP003_C12, of Exophiala spinifera isolate ESP002,
CC which encodes an amino polyol amine oxidase (APO, see AAY58902)
CC capable of degrading fumonisin, its hydrolysis product API, and
CC related mycotoxins. The DNA was obtained by PCR amplification of
CC ESP003 mycelial DNA using primers based on APO of E. spinifera
CC ATCC 74269. The invention provides APO polynucleotides (see
CC AAY58383-87) and polypeptides (see AAY58900-05) of E. spinifera and
CC Rhinocladia atrovirens. The polynucleotides are used to transform
CC plant cells normally susceptible to Fusarium or other toxin-producing
CC fungus infection. Transgenic plants can be regenerated from the

transformed plant cells. Also provided are methods for expressing both APAO and a fumonisin-esterase in a transgenic plant, and for producing APAO enzyme in prokaryotic and non-plant eukaryotic systems. Transgenic plants capable of degrading fumonisin or of producing the degrading enzymes are provided. Methods for detoxification of grain, grain processing, silage, food crops and in animal feed and rumen microorganisms are also disclosed. APAO polynucleotide is also useful as a selectable marker.

XX Sequence 1930 BP; 449 A; 531 C; 537 G; 412 T; 1 other;

Query Match 96.0%; Score 1851.4; DB 21; Length 1930;
Best Local Similarity 97.8%; Pred. No. 0;
Matches 1887; Conservative 0; Mismatches 42; Indels 1; Gaps 1;

QY 1 ATGGCATTGACCGAGCTACATCAATCCCAACCTCGCTCCCCAGCAGGGTATTCC 60
DB 1 ATGGCATTGACCGAGCTACATCAATCCCAACCTCGCTCCCCAGCAGGGTATTCT 60

QY 61 CACATCGCGGTAGGCCAAAGCGAGGATATGTGACAATAGCTGGACAGATTGGACAA 120
DB 61 CACGTGCGGTAGGCCAGAGCGAGGGAGGTATGTGACATAGCTGCACAGATTGGACAA 120

QY 121 GACGTTTGGCGGTGACAGACCGAGCTACGAGAAACAGGTTGCCCAAGCATTCGCCAAT 180
DB 121 GACGTTTGGCGGTGACAGACCGCTCCCTTACGAGAAACAGGTTGCCCAAGCATTCGCCAAT 180

QY 181 CTGCGAGCTTGCCTGTGTCAGTTGGAGCCCTTCAACGACGTCACCAAGCTCAATTAC 240
DB 181 CTGCGAGCTTGCCTGTGTCAGTTGGAGCCACTTCAACGACGTCACCAAGCTCAATTAC 240

QY 241 TACATCGTCGACTAGCCCGCAGCAAACTACCGCAATTTGAGATGGGCTGAAGTCTACC 300
DB 241 TACATCGTCGACTAGCCCGCAGCAAACTACCGCAATTTGAGATGGGCTGAAGGCTACC 300

QY 301 TTGTCCTTGCAGAGTCCCTTCTTGCAGCTGTGTCAGCTACCGGCTTGGGCTTACCT 360
DB 301 TTGTCCTTGCAGAGTCCCTTCTTGCAGCTGTGTCAGCTACCGGCTTGGGCTTACCT 360

QY 361 GAATACCTCTTGGATTGATGCCAGCGCTGGTGGCCAGACACTCGACCCAGACAAC 420
DB 361 GAATACCTCTTGGATTGATGCCAGCGCTGGTGGCCAGACACTCGACCCAGACAAC 420

QY 421 GTTGGGACGTGGTAGTGGTGGGCTGGCTTGGAGCGGTTTGGAGCGGCACGCAAAAGTC 480
DB 421 GTTGGGACGTGGTAGTGGTGGGCTGGCTTGGAGCGGTTTGGAGCGGCACGCAAAAGTC 480

QY 481 CAGGCGCGGCTGTCTGCTGCTGTCTTGGCGGATGGATCGTGTAGGGGGAAAGACT 540
DB 481 CAGGCGCGGCTGTCTGCTGCTGTCTTGGCGGATGGATCGTGTAGGGGGAAAGACT 540

QY 541 CTGAGCGTACAATCGGFTCCCGGAGGAGACTATCAACGACCTCGCGCTGCGTGGATC 600
DB 541 CTGAGCGTACAATCGGFTCCCGGAGGAGACTATCAACGACCTCGCGCTGCGTGGATC 600

QY 601 AATGACAGCAACCAAGCGAAGTATCCAGATTGTTGAAAGATTTCATTTGGAGGGCGAG 660
DB 601 AATGACAGCAACCAAGCGAAGTATCCAGATTGTTGAAAGATTTCATNTGGAGGGCGAG 660

QY 661 CTCGAGAGCAGCAGGAAATTCATTCATCAAGCACAAGACGGTACACCACTACAGCT 720
DB 661 CTCGAGAGCAGCAGGAAATTCATTCATCAAGCACAAGACGGTACACCACTACAGCT 720

QY 721 CCTTATGTTGACTCCCGGTGAGCAATCCCACTTTTGTGATGAGCTCTGTGAGTGT 780
DB 721 CCTTATGTTGACTCTTGGTAGCAATCCCACTTTTGTGATGAGCTCTGTGAGTGT 780

QY 781 AGAATACAGTCACTGACTCCACTTCGTCAGCTGAGCGAGGAGGTTGCAAGTGCACTTGC 840
DB 781 AGAATACAGTCACTGATTCACCTTCGTCAGCTGAGCGAGGAGGTTGCAAGTGCACTTGC 840

QY 841 GGAATCTCTCCCGTATGGTCTGAGCTGATCGAAGAGTATAGCCTTGAAGACCCCAAGGC 900
DB 841 GGAATCTCTCCCGTATGGTCTGAGCTGATCGAAGAGTATAGCCTTGAAGACCCCAAGGC 900

DB 841 GGAATCTCTCCCGTATGGTCTGAGCTGATCGAAGAGCATAGCCTTCAAGACCTCAAGGC 900

QY 901 GAGCCCTCAGGCGAAGCGCTCGACAGTGTGAGCTTCGCGCACTACTGTGTGAGAAGACT 960
DB 901 GAGCCCTCAGGCGAAGCGCTCGACAGTGTGAGCTTCGCGCACTACTGTGTGAGAAGACT 960

QY 961 AAACCTTGCCTGTGTTCTCAGCGTGGCAACAGATCACACGCGCTCTGCTCGGTGTGGA 1020
DB 961 AAACCTTGCCTGTGTTCTCGCGGTAGCAAAACAGATCACACGCGCTCTGCTCGGTGTGGA 1020

QY 1021 AGCCACAGAGATCAGCATGCTTTTCTCACCAGCTACATCAAGAGTGCACCGGTCTCAG 1080
DB 1021 AGCCACAGAGATCAGCATGCTTTTCTCACCAGCTACATCAAGAGTGCACCGGTCTCAG 1080

QY 1081 TAATATTGCTCGGACAAGAAAGACGGCGGAGTATATGCGATGCAAAACAGGTGCGGTG 1140
DB 1081 TAATATTGCTCGGACAAGAAAGACGGCGGAGTATATGCGATGCAAAACAGGTGCGGTG 1140

QY 1141 CGGTGCTCTCAGSTAGGGGACTCGTTTCT-TAGTGGTCAATTCAGAGTATCGAGTCGAT 1199
DB 1141 TGGTGTGCTCAGSTAGGGGACTCGTTTCTCAAGTGGTCAATTCAGAGTATCGAGTCGAT 1200

QY 1200 TTCCATGCCATGTCAAAGAACTTGTCCAGGCTCAGTGCAGCTCAACACCCCGTCCG 1259
DB 1201 TTGCCATGCCATGTCAAAGAACTTGTTCAGGCTCAGTGCAGCTCAACACCCCGTCCG 1260

QY 1260 TGGAAATTGAGCAGTCGCGCTGATAGTACGATCGGCTCGGGCGCGGTGTTCCG 1319
DB 1261 TGAATTGAGCAGTCGCGCTGATAGTACGATCGGCTCGGGCGCGGTGTTCCG 1320

QY 1320 AAGCAAAAAGGTGGTTCGTTACCGACAACATTTGATCCACCTTGACATTTTCACC 1379
DB 1321 AAGCAAAAAGGTGGTTCGTTACCGACAACCTTTGATCCACCTTGACATTTTCACC 1380

QY 1380 ACCTTCCCGCGAGAGCAAGCATTTGGCGAAATAATCTATCTCGGCTACTATAGCAA 1439
DB 1381 ACCTTCCCGCGAGAGCAAGCATTTGGCGAAATAATCTATCTCGGCTACTATAGCAA 1440

QY 1440 GATAGTCTTGTATGGACAACCCGTTGGCGCAACAAAGGCTTCGCGGCTCTCCCA 1499
DB 1441 GATAGTCTTGTATGGACAACCCGTTGGCGCAACAAAGGCTTCGCGGCTCTCCCA 1500

QY 1500 ATCAGCTGTGACCCCATCTCAATTTGCCAGAGATACAGCATCGAAGTCGATCGCAATG 1559
DB 1501 ATCAGCTGTGACCCCATCTCAATTTGCCAGAGATACAGCATCGAAGTCGATCGCAATG 1560

QY 1560 GTCCATTACCTGTTTATGTCGGAGACCCGGACGGAAGTGTGCCACAGTCCCAAGCA 1619
DB 1561 GTCCATTACCTGTTTATGTCGGAGACCCGGACGGAAGTGTGCCACAGTCCCAAGCA 1620

QY 1620 GGTACGACAAAAGTCTGTCTGGGACCAACTCCGCGCAGCTACGAGAAGCGCGGGCCCA 1679
DB 1621 GGTACGACAAAAGTCTGTCTGGGACCAACTCCGCGCAGCTACGAGAAGCGCGGGCCCA 1680

QY 1680 AGTCCGAGCGCGCTATATGGGCTGAACGATCTCATCACACTGGGTTGCGGCTCAGAAC 1739
DB 1681 AGTCCGAGCGCGCTATATGGGCTGAACGATCTCATCACACTGGGTTGCGGCTCAGAAC 1740

QY 1740 AGCTCCGAGCGCGCTATATGGGCTGAACGATCTCATCACACTGGGTTGCGGCTCAGAAC 1799
DB 1741 AGCTCCGAGCGCGCTATATGGGCTGAACGATCTCATCACACTGGGTTGCGGCTCAGAAC 1800

QY 1800 GCGTTCACAGTGTGTTCAATTCGTTGGAACGGAGCTCTTATAGTTTGAAGGGTATAT 1859
DB 1801 GCGTTCACAGTGTGTTCAATTCGTTGGAACGGAGCTCTTATAGTTTGAAGGGTATAT 1860

QY 1860 GGAAGGGCCATACGATTCGGGTCAACAGGTGCTGCAGAAGTTGTGGCTAGCCTGGTGC 1919
DB 1861 GGAAGGGCCATACGATTCGGGTCAACAGGTGCTGCAGAAGTTGTGGCTAGCCTGGTGC 1920

QY 1920 AGCAGCATAG 1929
DB 1921 AGCAGCATAG 1930

| | | Matches | 1850; | Conservative | 0; | Mismatches | 78; | Indels | 1; | Gaps | 1; |
|----|------|--|-------|--------------|----|------------|-----|--------|----|------|----|
| QY | 1 | ATGGCACTTGACCGAGCTACATCAATCCCCCAAAACGCTCGCTCCCGAGGATATTC | 60 | | | | | | | | |
| DB | 1 | ATGGCACTTGACCGAGCTACATCAATCCCCCAAAACGCTCGCTCCCGAGGATATTC | 60 | | | | | | | | |
| QY | 61 | CACATCGGCTAGGCCCAAAACGAGCGAGGTATGTGACAAATAGCTGGACAGATTGGACAA | 120 | | | | | | | | |
| DB | 61 | TACGTGCGGTAGGCCCAAAACGAGCGAGGTATGTGACAAATAGCTGGACAGATTGGACAA | 120 | | | | | | | | |
| QY | 121 | GACCTTTGGGCTGACAGACCCAGCCTACGAGAAACAGGTTGCCCAAGCATTTGCCAAT | 180 | | | | | | | | |
| DB | 121 | GACCTTTGGGCTGACAGACCCAGCCTACGAGAAACAGGTTGCCCAAGCATTTGCCAAT | 180 | | | | | | | | |
| QY | 181 | CTGGAGCTTGCCTTGCTGAGTTGGAGCTCTTCAACGACGCTCACCAAGCTCAATTAC | 240 | | | | | | | | |
| DB | 181 | CTGGAGCTTGCCTTGCTGAGTTGGAGCTCTTCAACGACGCTCACCAAGCTCAATTAC | 240 | | | | | | | | |
| QY | 241 | TACATCGTGACTACGCCCGGAGCAAACTCACCGCAATTGGAGATGGGTGAAGTCTACC | 300 | | | | | | | | |
| DB | 241 | TACATCGTGACTACGCCCGGAGCAAACTCACCGCAATTGGAGATGGGTGAAGTCTACC | 300 | | | | | | | | |
| QY | 301 | TTTGCCCTTGACAGGCTCCCTCTTGACACCTGGTGCCAGTACCGGCTTTGGCTTCACT | 360 | | | | | | | | |
| DB | 301 | TTTGCCCTTGACAGGCTCCCTCTTGACACCTGGTGCCAGTACCGGCTTTGGCTTCACT | 360 | | | | | | | | |
| QY | 361 | GAATACCTCTTTGAGGTTGATGCCACGGCGCTGTGTCAGGACACTCGACCCGAGACAAC | 420 | | | | | | | | |
| DB | 361 | GAATACCTCTTTGAGGTTGATGCCACGGCGCTGTGTCAGGACACTCGACCCGAGACAAC | 420 | | | | | | | | |
| QY | 421 | GTTCGGGAGCTGTGTGTTGGGCGCTGGCTTGAGCGGTTTGGAGACGGCACCAAGTC | 480 | | | | | | | | |
| DB | 421 | GTTCGGGAGCTGTGTGTTGGGCGCTGGCTTGAGCGGTTTGGAGACGGCACCAAGTC | 480 | | | | | | | | |
| QY | 481 | CAGCCCGCGGCTCTGCTCCTCGCTCGTCTTGAGGCGATGATCGTGTAGGGGAAAGACT | 540 | | | | | | | | |
| DB | 481 | CAGCTCGCGGCGTCTGCTCCTCGCTCGTCTTGAGGCGATGATCGTGTAGGGGAAAGACT | 540 | | | | | | | | |
| QY | 541 | CTGAGCGTACAATCGGGTCCCGGAGGACGACTATCAACGACCTCGCGCGCTGGTGATC | 600 | | | | | | | | |
| DB | 541 | CTGAGCGTACAATCGGGTCCCGGAGGACGACTATCAACGACCTCGCGCGCTGGTGATC | 600 | | | | | | | | |
| QY | 601 | AATGACAGCAACCAAGCGAAGTATCCAGATTGTTTGAAGATTTCATTTGGAGGCGGAG | 660 | | | | | | | | |
| DB | 601 | AATGACAGCAACCAAGCGAAGTATCCAGATTGTTTGAAGATTTCATTTGGAGGCGGAG | 660 | | | | | | | | |
| QY | 661 | CTCAGAGGAGCAGCCGGAATTCATCCATCAAGCACAGACGGTACACCACACTACAGCT | 720 | | | | | | | | |
| DB | 661 | CTCAGAGGAGCAGCCGGAATTCATCCATCAAGCACAGACGGTACACCACACTACAGCT | 720 | | | | | | | | |
| QY | 721 | CCTTATGGTGAATCCCGGTAAGCAATCCCACTTTGTGATGAGACCTCTGTGCGAGTGT | 780 | | | | | | | | |
| DB | 721 | CCTTATGGTGAATCCCGGTAAGCAATCCCACTTTGTGATGAGACCTCTGTGCGAGTGT | 780 | | | | | | | | |
| QY | 781 | AGAATACAGTCACTGACTCCACTTCCAGCTGAGCGAGGAGTTGCAAGTGCATCTCC | 840 | | | | | | | | |
| DB | 781 | AGAATACAGTCACTGACTCCACTTCCAGCTGAGCGAGGAGTTGCAAGTGCATCTCC | 840 | | | | | | | | |
| QY | 841 | GGAACCTCTCCCGTATGGTCTCAGCTGATCGAGAGTATAGCTTTGAAGACCCCAAGGC | 900 | | | | | | | | |
| DB | 841 | GGAACCTCTCTCCCGCATGGTCTCAGCTGATCGAGAGTATAGCTTTGAAGACCCCAAGGC | 900 | | | | | | | | |
| QY | 901 | GAGCCCTCAGGCGAAGCGGCTCCACAGTGTGAGCTTCGCGCACTACTGTGAGAAGGACT | 960 | | | | | | | | |
| DB | 901 | GAGCCCTCAGGCGAAGCGGCTCCACAGTGTGAGCTTCGCGCACTACTGTGAGAAGGACT | 960 | | | | | | | | |
| QY | 961 | AAACTTGCCTGTGTTCTCAGCGTGCGCAACACAGATFACACGCGCTCTCCTCGGTGTGA | 1020 | | | | | | | | |
| DB | 961 | AAACTTGCCTGTGTTCTCAGCGTGCGCAACACAGATFACACGCGCTCTCCTCGGTGTGA | 1020 | | | | | | | | |
| QY | 1021 | AGCCACAGGATCAGCATGCTTTTCTCAGCCGCTACATCAAGAGTGCCACCGGCTCAG | 1080 | | | | | | | | |
| DB | 1021 | AGCCACAGGATCAGCATGCTTTTCTCAGCCGCTACATCAAGAGTGCCACCGGCTCAG | 1080 | | | | | | | | |

RESULT 4
AAZ58386
ID AAZ58386 standard; DNA; 1928 BP.
XX
AC AAZ58386;
XX
DT 23-MAY-2000 (first entry)
XX
DE Rhinocladiaella atrovirens amino polyol amine oxidase RAT011-C2 DNA.
XX
KW Amino polyol amine oxidase; funonisln; mycotoxin; transgenic plant;
KW detoxification; animal feed; silage; selectable marker; ds.
XX
OS Rhinocladiaella atrovirens.
XX
FH Key Location/Qualifiers
FT CDS 1..1928
FT /tag= a
FT /note= "contains introns"
FT Intron 739..811
FT /tag= b
FT Intron 1134..1186
FT /tag= c
XX
PN WO200004159-A1.
XX
PD 27-JAN-2000.
XX
PF 08-JUL-1999; 99WO-US15454.
XX
PR 15-JUL-1999; 98US-0092936.
PR 21-MAY-1999; 98US-0135391.
XX
PA (PION-) PIONEER HI-BRED INT INC.
PA (CURA-) CURAGEN CORP.
XX
PI Duvick JP, Gilliam JT, Maddox JR;
XX
XX WPI; 2000-182425/16.
DR P-PSDB; AAY58904.
XX
XX New isolated polynucleotides, polypeptides useful for detecting and
PT degrading fumonisln or structurally related mycotoxin in processed
PT grain or in silage
XX
PS Claim 1; Page 145-146; 154pp; English.
XX
XX The present sequence is that of an isolated nucleic acid,
CC designated RAT011-C2, of Rhinocladiaella atrovirens isolate RAT011,
CC which encodes an amino polyol amine oxidase (APAO, see AAY58904),
CC capable of degrading fumonisln, its hydrolysis product APl, and
CC related mycotoxins. The DNA was obtained by PCR amplification of
CC RAT011 mycelial DNA using primers based on APAO of E. spinifera
CC ATCC 74269. The invention provides APAO polynucleotides (see
CC AAY58383-87) and polypeptides (see AAY58900-05) of R. atrovirens and
CC Exophiala spinifera. The polynucleotides are used to transform
CC plant cells normally susceptible to Fusarium or other toxin-producing
CC fungus infection. Transgenic plants can be regenerated from the
CC transformed plant cells. Also provided are methods for expressing
CC both APAO and a fumonisln-esterase in a transgenic plant, and for
CC producing APAO enzyme in prokaryotic and non-plant eukaryotic
CC systems. Transgenic plants capable of degrading fumonisln or of
CC producing the degrading enzymes are provided. Methods for
CC detoxification of grain, grain processing, silage, food crops and
CC in animal feed and rumen microorganisms are also disclosed. APAO
CC polynucleotide is also useful as a selectable marker.
XX
SQ Sequence 1928 BP; 450 A; 527 C; 534 G; 417 T; 0 other;
Query Match 92.9%; Score 1792.2; DB 21; Length 1928;
Best Local Similarity 95.9%; Pred. No. 0;

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QY 1081 TAATATTGTCGGACAGAAGACGGCGCAGTATATGCGATGCAAAACAGGTGCGTG 1140
DB 1081 TAATATTGTCGATRAGAAGACGGTGGCAGTATATGCGATGCAAAACAGGTGCGTG 1140
QY 1141 CGGTGCTCTCAGGTAGGGACCTCGTTCTTCTAGTGTCTATCCAGGTATGCAGTCGATT 1200
DB 1141 TGGTGTCTCTCTCA-GTGGAGACTCGTTCTTCTAGTGTCTATCCAGGTATGCAGTCGTT 1199
QY 1201 TGGCATGCATGTCAAAGAACTTGTCCAGGCTCACTGCACCTCAACACGCCGCTGCT 1260
DB 1200 TGGCATGCATGTCAAAGAACTTGTCCAGGCTCACTGCACCTCAACACGCCGCTGCTG 1259
QY 1261 GGAATTGAGCAGTCGGCTCGGCTGTATAGTACGATCGGCTCGGCGCGCTGTTCCGA 1320
DB 1260 GAAATTGAGCAGTCGGCTCGGCTGTACAGTACGATCGGCTCGGCGCGCTGTTCCGA 1319
QY 1321 AGCAAAAAGGTGGTGTTCCTTACCGACAACATTTATGCCACCTTGAATTTTACCA 1380
DB 1320 AGTAAAAAGGTGGTGTTCCTTACCGACAACCTTGTATCCACCTTGATATTTTACCA 1379
QY 1381 CCTCTTCCCGCGGAGAACAGCATTCGCGAAAATCTATCCTCGCTACTATAGCAAG 1440
DB 1380 CCTCTTCCCGCGGAGAACAGCATTCGCTGAAAATCTATCCTCGCTACTATAGCAAG 1439
QY 1441 ATAGTCTTTCGTATGGACAACCCGTGGTGGCGGAACAAAGGCTTCTCGGGCGTCTCTCAA 1500
DB 1440 ATAGTCTTTCGTATGGACAACCCGTGGTGGCGGAACAAAGGCTTCTCGGGCGTCTCTCAA 1499
QY 1501 TCGAGCTGTACCCCATCTCATTTGCCAGAGATACCAAGCATCGAAGTCGATCGGCAATGG 1560
DB 1500 TCGAGCTGTACCCCATCTCATTTGCCAGAGATACCAAGCATCGAAGTCGATCGGCAATGG 1559
QY 1561 TCCATTACCTCTTTCATGCTCGGAGACCCGGACGGAGTGGTCCCAACAGTCCCAACGAG 1620
DB 1560 TCCATTACCTCTTTCATGCTCGGAGACCCGGACGGAGTGGTCCCAACAGTCCCAACGAG 1619
QY 1621 GTACGACAAAAGTCTGTCTGGGACCACTCGCGCAGCCTACGAGAACCGCGGGGCCCAA 1680
DB 1620 GTACGACAGAAGTCTGTCTGGAACCACTCGCGCAGCCTACGAGAACCGCGGGGCCCAA 1679
QY 1681 GTCCAGAGCGCGCAACGCTGCTGAAATCAGTGGTGGAGAGCAGCATATTTCCAAAGGA 1740
DB 1680 GTCCAGAGCGCGCAACGCTGCTGAGATCAGTGGTGGAGAGCAGCATATTTCCAAAGGA 1739
QY 1741 GCTCGAGCGCGCTATGGCTGAACGATCTCATCAGCTGGCTCGGCGCTCAGAACG 1800
DB 1740 GCGCGAGCGCGCTATGGCTGAACGATCTCATCAGCTGGCTCGGCGCTCAGAACG 1799
QY 1801 CGGTTCAAGTGTGTTTTCGTTGGAACGGAGACGCTCTTTAGTTTGAAGGGTATATG 1860
DB 1800 CGGTTCAAGGGTGTTCATTTCTGTTGGAACGGAGACGCTCTTTGTTTGAAGGGTATATG 1859
QY 1861 GAAGGGCCATACGATCGGGTCAACAGAGTCTCGAAGAGTTGGTGTAGCTGGTGCCA 1920
DB 1860 GAAGGGCCATACGATCGGGTCAACAGAGTCTCGAAGAGTTGGTGTAGCTGGTGCCA 1919
QY 1921 GCAGCATAG 1929
DB 1920 GCAGCATAG 1928

RESULT 5
AAZ58387
ID AAZ58387 standard; DNA; 1928 BP.
XX
AC AAZ58387;
XX
DT 23-MAY-2000 (first entry)
XX
DE Rhinocladiaella atrovirens amino polyol amine oxidase RAT011-C4 DNA.
XX
KW Amino polyol amine oxidase; funonisin; mycotoxin; transgenic plant;
```

```
KW detoxification; animal feed; silage; selectable marker; ds.
XX Rhinocladiaella atrovirens.
XX
FH Key Location/Qualifiers
FT CDS 1..1928
FT /tag= a
FT /note= "contains introns"
FT intron 739..811
FT /tag= b
FT intron 1134..1185
FT /tag= c
XX
PN WO200004159-A1.
XX
XX 27-JAN-2000.
XX
XX 08-JUL-1999; 99WO-US15454.
XX
XX 15-JUL-1998; 98US-0092936.
XX 21-MAY-1999; 99US-0135391.
XX
XX (PION-) PIONEER HI-BRED INT INC.
XX (CURA-) CURAGEN CORP.
XX
XX Duvick JP, Gilliam JT, Maddox JR;
XX
XX WPI: 2000-182425/16.
XX P-PSDB; AAY58905.
XX
XX New isolated polynucleotides, polypeptides useful for detecting and
PT degrading funonisin or structurally related mycotoxin in processed
PT grain or in silage
PT
XX
PS Claim 1; Page 147-148; 154pp; English.
XX
XX The present sequence is that of an isolated nucleic acid,
CC designated RAT011-C4, of Rhinocladiaella atrovirens isolate RAT011,
CC which encodes an amino polyol amine oxidase (AAPO, see AAY58905)
CC capable of degrading funonisin, its hydrolysis product AP1, and
CC related mycotoxins. The DNA was obtained by PCR amplification of
CC RAT011 mycelial DNA using primers based on AAPO of E. spinifera
CC ATCC 74269. The invention provides AAY58900-05) of R. atrovirens and
CC AAZ58383-87) and polypeptides (see AAY58900-05) of R. atrovirens and
CC Exophiala spinifera. The polynucleotides are used to transform
CC plant cells normally susceptible to Fusarium or other toxin-producing
CC fungus infection. Transgenic plants can be regenerated from the
CC both AAPO and a funonisin-esterase in a transgenic plant, and for
CC producing AAPO enzyme in prokaryotic and non-plant eukaryotic
CC systems. Transgenic plants capable of degrading funonisin or of
CC producing the degrading enzymes are provided. Methods for
CC detoxification of grain, grain processing, silage, food crops and
CC in animal feed and rumen microorganisms are also disclosed. AAPO
CC polynucleotide is also useful as a selectable marker.
XX
SQ Sequence 1928 BP; 449 A; 528 C; 534 G; 417 T; 0 other;
```

```
Query Match 92.7%; Score 1789; DB 21; Length 1928;
Best Local Similarity 95.8%; Pred. No. 0;
Matches 1848; Conservative 0; Mismatches 80; Indels 1; Gaps 1;

QY 1 ATGGCACTTGACCGAGCTACATCAATCCCAAGCTGCGCTCCCGACAGGGTATTC 60
DB 1 ATGGCACTTGACCGAGCTACATCAATCCCAAGCTGCGCTCCCGACAGGGTATTC 60
QY 61 CACATCGGCTAGGCGCCAAACGAGGAGGTATGTGACAAATAGCTGGACAGATTGGACAA 120
DB 61 CACGTCGGCTAGGCCCAACGAGGAGGAGGTATGTGACAAATAGCTGGACAGATTGGACAA 120
QY 121 GAGCGTTTGGCGGTGACAGACCGAGCTACGAGAAACAGGTTGCCCAAGCATTCGCAAT 180
DB 121 GAGCGTTTGGCGGTGACAGACCGAGCTACGAGAAACAGGTTGCCCAAGCATTCGCAAC 180
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PN WO200004159-A1.
XX 27-JAN-2000.
XX 08-JUL-1999; 99WO-US15454.
XX 15-JUL-1998; 98US-0092936.
PR 21-MAY-1999; 99US-0135391.
XX (PION-) PIONEER HI-BRED INT INC.
PA (CURA-) CURAGEN CORP.
PI Duwick JP, Gilliam JT, Maddox JR;
XX WPI; 2000-182425/16.
DR P-PSDB; AAY58903.
XX
PT New isolated polynucleotides, polypeptides useful for detecting and
PT degrading fumonisins or structurally related mycotoxin in processed
PT grain or in silage
XX
PS Claim 1; Page 143-44; 154pp; English.
XX
CC The present sequence is that of an isolated nucleic acid,
CC designated RAT011-Cl, of *Rhizoctonia* isolate RAT011,
CC which encodes an amino polyol amine oxidase (APO, see AAY58903)
CC capable of degrading fumonisin, its hydrolysis product AP1, and
CC related mycotoxins. The DNA was obtained by PCR amplification of
CC RAT011 mycelial DNA using primers based on APO of *E. spinifera*
CC ATCC 74269. The invention provides APO polynucleotides (see
CC AAY58903-87) and polypeptides (see AAY58900-05) of *R. atroviens* and
CC *Exophiala spinifera*. The polynucleotides are used to transform
CC plant cells normally susceptible to Fusarium or other toxin-producing
CC fungus infection. Transgenic plants can be regenerated from the
CC transformed plant cells. Also provided are methods for expressing
CC both APO and a fumonisin-esterase in a transgenic plant, and for
CC producing APO enzyme in prokaryotic and non-plant eukaryotic
CC systems. Transgenic plants capable of degrading fumonisin or of
CC producing the degrading enzymes are provided. Methods for
CC detoxification of grain, grain processing, silage, food crops and
CC in animal feed and rumen microorganisms are also disclosed. APO
CC polynucleotide is also useful as a selectable marker.
XX
SQ Sequence 1928 BP; 448 A; 530 C; 536 G; 414 T; 0 other;

Query Match 92.7%; Score 1787.4; DB 21; Length 1928;
Best Local Similarity 95.7%; Pred. No. 0;
Matches 1847; Conservative 0; Mismatches 81; Indels 1; Gaps 1;

QY 1 ATGGCACTTGACCGAGTACATCAATCCCCAAACGCTCGCCTCCCGCAGCAGGATATTC 60
DB 1 ATGGCACTTGACCGAGTACATCAATCCCCAAACGCTCGCCTCCCGCAGCAGGATATTC 60
QY 61 CACATCGCGGTAGGCCCAACAGAGCGAGGTATGTGACAAATAGTGGACAGATTTGGACAA 120
DB 61 CACGTCGGCGTAGGCCCAACAGAGCGAGGTATGTGACAAATAGTGGACAGATTTGGACAA 120
QY 121 GACGCTTTGGCGGTGACAGACCCAGCTTACAGAAACAGGTTGCCAGAGCATTCGCCAAT 180
DB 121 GACGCTTTGGCGGTGACAGACCCAGCTTACAGAAACAGGTTGCCAGAGCATTCGCCAAT 180
QY 181 CTGCGAGCTTGCTGCTGCGAGTTGGAGCTCTTCAACACAGCTCAGCAAGCTCAATTTAC 240
DB 181 CTGCGAGCTTGCTGCTGCGAGTTGGAGCTCTTCAACACAGCTTACCAAGCTCAATTTAC 240
QY 241 TACATCGTGCATAGCCCGGAGCAAACTACCGCAATTTGGAGATGGGCTGAAGCTTACC 300
DB 241 TACATCGTGCATAGCAACCCGAGCAAACTACCGCAATTTGGAGATGGGCTGAAGGCTACC 300
QY 301 TTTGCCCTTGACAGGCTCCCTTGTGACGCTGGTGCAGTACCGGCTTGGCTTACCT 360
DB 301 TTTGCCCTTGACAGGCTCCCTTGTGACGCTGGTGCAGTACCGGCTTGGCTTACCT 360

QY 361 GAATACCTCTTTGAGCTTGATGCCACGGCGCTGGTCCAGGACACTCGACCCGACAAAC 420
DB 361 GAATACCTCTTTGAGCTTGATGCCACGGCGCTGGTCCAGGACACTCAACCCGACAAAC 420
QY 421 GTTGGCGAGCTGTAGTGGCGCTGGCTTGAGCGGTTTGAGACGCGACGCAAAAGTC 480
DB 421 GTTGGCGAGCTGTAGTGGCGCTGGCTTGAGCGGTTTGAGACGCGACGCAAAAGTC 480
QY 481 CAGCGCGCGCTGTCTCCCTCGCTTCTTGGAGCGATGATCGTGTAGGGGGAAGACT 540
DB 481 CAGCGCTGCCGGCTGTCTCCCTCGCTTCTTGGAGCGATGATCGTGTGGGGGAAGACT 540
QY 541 CTGAGGCTACAATCGGGTCCCGCAGGAGGACTATCAACGAGCTCGGCGCTCGCTGGATC 600
DB 541 CTGAGGCTACAATCGGGTCCCGCAGGAGGACTATCAATGACCTCGGCGCTCGCTGGATC 600
QY 601 AATGACAGCAACCAAGCGAAGTATCCGATTTGTTTGAAGATTTCAATTTGGAGGCGAG 660
DB 601 AATGACAGCAACCAAGCGAAGTATTTCAAAATTTATTTGAAAGATTTCAATTTGGAGGCGAG 660
QY 661 CTCCAGGAGGACCGGAAATTCATCCATCAGCACAGAGGCTACACCACTACAGCT 720
DB 661 CTCCAGGAGGACCGGAAATTCATCCATCAGCACAGAGGCTACACCACTACAGCT 720
QY 721 CCTATGGTGACTCCCGGTAAGCAACAATCCCACTTTGTGATGAGACCTCTCTCGAGTGT 780
DB 721 CCTATGGTGATTCCTCGTGTGAGCAACAATCCATCTTGTGATGAGACCTCTCTCGTGTGT 780
QY 781 AGAATACAGTCACTACTCCACTTCCTCAGCTGAGCGAGGTTTGAAGTGCATTTGC 840
DB 781 AGAATACAGTCACTACTCCACTTCCTCAGCTGAGCGAGGTTTGAAGTGCATTTGC 840
QY 841 GGAACCTCTCCCGTATGTCTCAGCTGATCAGAGAGTATAGCTTGAAGACCCCAAGC 900
DB 841 GGAACCTCTCCCGATGTGTCTCAGCTGATCAGAGAGTATAGCTTGAAGACCCCAAGC 900
QY 901 GAGCCCTCAGCGAAGCGGCTGCACAGTGTGAGCTTCGCGCACTACTGTGAGAAGGACT 960
DB 901 GAGCCCTCAGCGAAGCAGCTGCACAGTGTGAGCTTCGCGCACTACTGTGAGAAGGACT 960
QY 961 AACTTGCCTGTCTCAGCTGCGAACCAGATCACACGCGCTCTCTCGGTGTGA 1020
DB 961 AAGCTTGCCTGTCTCTCGCGTGGCAACCAGATCACACGCGCTCTCTCGGTGTGA 1020
QY 1021 AGCCACGAGATCAGCATGCTTTTCTCAGCGACTACATCAAGCTGCCAGTCCAG 1080
DB 1021 AGCCACGAGATCAGCATGCTTTTCTCAGCGACTACATCAAGCTGCCAGTCCAG 1080
QY 1081 TAATATTGTCTCGGACAAGAACGCGCGGAGTATATCGATGCAAAACAGGTCGCTG 1140
DB 1081 TAATATTGTCTCGGATAGAAAGACCGGTGGCAGTATATCGGATGCAAAACAGGTCGCTG 1140
QY 1141 CGGTGCTCTCAGGTAGGAGACTCGTTTCTTAGTGGTCAATTCAGGTATGAGTGCATT 1200
DB 1141 TGGTGTCTCTCA - GTGGGAGACTCGTTTCTTAGTGGTCAATTCAGGTATGAGTGCCTT 1199
QY 1201 TGCCATGCCATGTCAAGGAGTGTTCAGGCTCAGTGCACCTCAACACCCCGCTCGCT 1260
DB 1201 TGCCATGCCATGTCAAGGAGTGTTCAGGCTCAGTGCACCTCAACACCCCGCTCGCT 1260
QY 1261 GGAATTGAGCAGTCGGCGTCCGCTGTATAGTACGATCGGCTCGGCGCGCTGTTCCGA 1320
DB 1261 GGAATTGAGCAGTCGGCGTCCGCTGTATAGTACGATCGGCTCGGCGCGCTGTTCCGA 1320
QY 1321 AGCAAAAGTGTGTGTTTGGTTACCGACAACATTTGATCCCACTTTGACATTTTCAACA 1380
DB 1321 AGTAAAAAGTGTGTGTTTGGTTTACCGACAACCTTGTATCCCACTTTGATATTTCAACA 1379
QY 1381 CTTCTTCCCGCCGAGAGGAGCAATTTGGCGGGAATAATCTATCCTCGGCTACTATAGCAAG 1440
DB 1381 CTTCTTCCCGCCGAGAGGAGCAATTTGGCTGAAAAATCCATCCTCGGCTACTATAGCAAG 1439
QY 1441 ATAGTCTCTGATGGGACAACCGCTGTGGCGGCAACAAAGGCTTCTCGGGCGCTCTCCAA 1500

|||||
Db 1440 ATAGTCTTCGTATGGCAAGCCGTTGGCGGCAAGAGCTTCTCGGGGCTCCTCAA 1499
QY 1501 TCGAGCTGTGACCCCATCTCATTTCCAGAGATACACAGATCGAAGTCGATCGGCAATGG 1560
Db 1500 TCGAGCTGTGACCCCATCTCATTTCCAGAGATACACAGATCGAAGTCGATCGGCAATGG 1559
QY 1561 TCCATTACCTGTTTCATGTCGGAGACCCGGGAGGAAAGTGGTCCCAACAGTCCCAAGCAG 1620
Db 1560 TCCATTACCTGTTTCATGTCGGAGACCCGGGAGGAAAGTGGTCCCAACAGTCCCAAGCAG 1619
QY 1621 GTACGACAAAAGTCTGTCTGGGACCAACTCCGGCAGCCTACGAGAACGCCGGGCCCAA 1680
Db 1620 GTACGACAAAAGTCTGTCTGGAAACCAACTCCGGCAGCCTACGAGAACGCCGGGCCCAA 1679
QY 1681 GTCCAGAGCCGGCCAAAGTGTCTGAAATCGAGTGGTGCAGAGCAGCAGTATTTCCAAAGGA 1740
Db 1680 GTCCAGAGCCGGCCAAAGTGTCTGAGATCGAGTGGTGCAGAGCAGCAGTATTTCCAAAGGA 1739
QY 1741 GTCGAGCGCGCTATATGGGTGAACGATCTCATACACTGGGTTCGGCGCTCAGAAGC 1800
Db 1740 GCGCGAGCGTCTATATGGGTGAACGTCTCAACACACTGGGTTCGGCGCTCAGAAGC 1799
QY 1801 CCGTTCAAGTGTTTCATTCTGTTGGAACGAGACGCTTTAGTTTGGAAAGGCTATATG 1860
Db 1800 CCGTTCAAGGGTGTTCATTCTGTTGGAACGAGACGCTTTGGTTTGGAAAGGCTATATG 1859
QY 1861 GAAGGGGCATACGATCGGGTCAACGAGGTGCTGCAGAAAGTTGTGGCTTAGCCTGGTGCCA 1920
Db 1860 GAAGGGGCATACGATCGGGTCAACGAGGTGCTGCAGAAAGTTGTGGCTTAGCCTGGTGCCA 1919
QY 1921 GCAGCATAG 1929
Db 1920 GCAGCATAG 1928

RESULT 7
AAZ58402
ID AA258402 standard; cDNA; 1803 BP.
XX
AC AAZ58402;
XX
DT 23-MAY-2000 (first entry)
XX
DE Exophiala spinifera amino polyol amine oxidase cDNA.
XX
KW Amino polyol amine oxidase; fumonisin; mycotoxin; transgenic plant;
KW detoxification; animal feed; silage; selectable marker; ds.
XX
OS Exophiala spinifera.
XX
PN WO200004159-A1.
XX
PD 27-JAN-2000.
XX
PF 08-JUL-1999; 99WO-US15454.
XX
PR 15-JUL-1998; 98US-0092936.
PR 21-MAY-1999; 99US-0135391.
XX
PA (PION-) PIONEER HI-BRED INT INC.
PA (CURA-) CURAGEN CORP.
XX
PI Duwick JP, Gilliam JT, Maddox JR;
XX
DR WPI; 2000-182425/16.
DR P-PSDB; AAY58913.
XX
PT New isolated polynucleotides, polypeptides useful for detecting and
PT degrading fumonisin or structurally related mycotoxin in processed
PT grain or in silage
XX
PS Example 10; Page 97-100; 154pp; English.

XX The present sequence is that of the coding region of full-length
CC amino polyol amine oxidase (APAO) cDNA of Exophiala spinifera
CC 2141.10. APAO is capable of degrading fumonisin, its hydrolysis
CC product APL, and related mycotoxins. The invention provides APAO
CC polynucleotides (see AAY58383-87) and polypeptides (see AAY58900-05) of
CC E. spinifera and Rhinocladia atrovirens. The polynucleotides are
CC used to transform plant cells normally susceptible to Fusarium or
CC other toxin-producing fungus infection. Transgenic plants can be
CC regenerated from the transformed plant cells. Also provided are
CC methods for expressing both APAO and a fumonisin-esterase in a
CC transgenic plant, and for producing APAO enzyme in prokaryotic and
CC non-plant eukaryotic systems. Transgenic plants capable of degrading
CC fumonisin or of producing the degrading enzymes are provided.
CC Methods for detoxification of grain, grain processing, silage, food
CC crops and in animal feed and rumen microorganisms are also disclosed.
CC APAO polynucleotide is also useful as a selectable marker.
XX
SQ Sequence 1803 BP; 424 A; 501 C; 502 G; 376 T; 0 other;

Query Match 83.1%; Score 1602.6; DB 21; Length 1803;
Best Local Similarity 91.7%; Pred. No. 0;
Matches 1769; Conservative 0; Mismatches 34; Indels 126; Gaps 2;

QY 1 ATGGCACTTGACCGAGCTACATCAATCCCCAAACGTCCCTCCCCAGCAGGTATTC 60
Db 1 ATGGCACTTGACCGAGCTACATCAATCCCCAAACGTCCCTCCCCAGCAGGTATTC 60

QY 61 CACATCGGCGTAGCGCCCAACGAGGAGTATGTACAAATAGCTGGACAGATTGACAA 120
Db 61 CAGTCGGCGTAGCGCCACAGCGGAGGAGTATGTACAAATAGCTGGACAGATTGACAA 120

QY 121 GACGCTTTTGGGCGTGACAGACCAGCCTACGAGAAACAGGTTGCCCAAGCATTCGGCAAT 180
Db 121 GACGCTTCGGGCGTGACAGACCCTGCCTACGAGAAACAGGTTGCCCAAGCATTCGGCAAT 180

QY 181 CTGCGAGCTTGCCTTGCCTGAGTTGGAGCCTCTTCAAACGAGCTACCAAGCTCAATTAC 240
Db 181 CTGCGAGCTTGCCTTGCCTGAGTTGGAGCCTCTTCAAACGAGCTACCAAGCTCAATTAC 240

QY 241 TACATGCTGACTACGCCGAGCAAACTACCGCAATTTGGAGATGGGCTGAAGTCTACC 300
Db 241 TACATGCTGACTACGCCGAGCAAACTACCGCAATTTGGAGATGGGCTGAAGTCTACC 300

QY 301 TTTGCCCTTGACAGGCTCCCTCCTTGACGCTGGTGCCAGTACCGGCCCTTGGCTCACCT 360
Db 301 TTTGCCCTTGACAGGCTCCCTCCTTGACGCTGGTGCCAGTGTCCGCCCTTGTCTTCACT 360

QY 361 GAATACCTCTTTGAGGTTGATGCCACGGGCTGGTGCCAGGACACTCGACCCAGACAA 420
Db 361 GAATACCTCTTTGAGGTTGATGCCACGGGCTGGTGCCGGGACACACAGCCCCAGACAA 420

QY 421 GTATCGGAGCTGTAGTGGGCGCTGGCTTGAGCGGTTTGGAGACGCGACGCAAGTC 480
Db 421 GTTGGGAGCTGTAGTGGGCGCTGGCTTGAGCGGTTTGGAGACGCGACGCAAGTC 480

QY 481 CAGGCGCGCGCTGTCTCCTCCTCTTGTAGGGCATGGATCGTGTAGGGGAAAGACT 540
Db 481 CAGGCGCGCGCTGTCTCCTCCTCTTGTAGGGCATGGATCGTGTAGGGGAAAGACT 540

QY 541 CTGAGCGTACATCGGGTCCCGGAGGACTATCAACGACCTCGGCGCTCGTGGGATC 600
Db 541 CTGAGCGTACATCGGGTCCCGGAGGAGTATCAACGACCTCGGCGCTCGTGGGATC 600

QY 601 AATGACAGCAACCAAGCAAGTATCCAGATTGTTTGAAGATTTCATTTGAGGCGGAG 660
Db 601 AATGACAGCAACCAAGCAAGTATCCAGATTGTTTGAAGATTTCATTTGAGGCGGAG 660

QY 661 CTCAGAGGACGACCGGAAATTCATTCCTCAAGCAACAGCGGTACAACTACTACAGCT 720
Db 661 CTCAGAGGACGACTGAAATTCATTCCTCAAGCAACAGCGGTACAACTACTACAGCT 720

QY 721 CCTTATGGTGACTCCCGGTAAGCAACATCCCACTTTGTGATGAGACCTCTCTGCGAGTGT 780

QY 1 ATGGCACTTGCACCGAGCTACATCAATCCCAAGAGTGCCTCCCAAGAGGGATTCC 60
DB 1 ATGGCACTTGCACCGAGCTACATCAATCCCAAGAGTGCCTCCCAAGAGGGATTCT 60
QY 61 CACATCGGCGTAGGCCCAACGAGCGAGGTATGTGACAATAGCTGGACAGATTGGACAA 120
DB 61 CACGTGGGCGTAGGCCCAACGAGCGAGGAGGTATGTGACAATAGCTGGACAGATTGGACAA 120
QY 121 GAGCCTTTGGGCGTGACAGACCCAGCCTACGAGAAACAGTTGGCCCAAGCAATCCCAAT 180
DB 121 GAGCCTTTGGGCGTGACAGACCCAGCCTACGAGAAACAGTTGGCCCAAGCAATCCCAAT 180
QY 181 CTGCGAGCTTGCCCTGCTCAGTTGAGGCTCTTCAAAAGAGGTACCAAGCTCAATTAC 240
DB 181 CTGCGAGCTTGCCCTGCTCAGTTGAGGCTCTTCAAAAGAGGTACCAAGCTCAATTAC 240
QY 241 TACATCGTCGACTACGCCCGGAGCAACATCAGCGCAATTTGGAGATGGGTGAAGTCTACC 300
DB 241 TACATCGTCGACTACGCCCGGAGCAACATCAGCGCAATTTGGAGATGGGTGAAGTCTACC 300
QY 301 TTGCGCCTTGACAGGCTCCCTCCTTGCACGCTGGTGCCAGTACCGGCCCTTGCTTCACT 360
DB 301 TTGCGCCTTGACAGGCTCCCTCCTTGCACGCTGGTGCCAGTACCGGCCCTTGCTTCACT 360
QY 361 GAATACCTCTTTGAGGTTGATGCGAGGCGCTGGTGCCAGGACATCGACCCCAAGCAAC 420
DB 361 GAATACCTCTTTGAGGTTGATGCGAGGCGCTGGTGCCAGGACATCGACCCCAAGCAAC 420
QY 421 GTTGGCGAGCTGGTAGTGGTGGGCGCTGCTTGGAGCGATGGATCGTAGGGGGAAGACT 480
DB 421 GTTGGCGAGCTGGTAGTGGTGGGCGCTGCTTGGAGCGATGGATCGTAGGGGGAAGACT 480
QY 481 CAGGCGCGCGGCTGTCCTCCTTGTGAGCGATGGATCGTAGGGGGAAGACT 540
DB 481 CAGGCGCGCGGCTGTCCTCCTTGTGAGCGATGGATCGTAGGGGGAAGACT 540
QY 541 CTGAGGCTACATCGGCTCCCGGAGGAGGACTATCAAGGACCTCGGCGCTGCTGGATC 600
DB 541 CTGAGGCTACATCGGCTCCCGGAGGAGGACTATCAAGGACCTCGGCGCTGCTGGATC 600
QY 601 AATGACGACCAACAAAGCAAGTATCCAGATGTTTGAAGATTTCATTTGAGGGCCAG 660
DB 601 AATGACGACCAACAAAGCAAGTATCCAGATGTTTGAAGATTTCATTTGAGGGCCAG 660
QY 661 CTCGAGAGGACACCGGAAATTCATCCATCAAGCACAGAGGTAACACCACTACAGCT 720
DB 661 CTCGAGAGGACACTGGAATTCATCCATCAAGCACAGAGGTAACACCACTACAGCT 720
QY 721 CCTTATGGTGAATCCCGGTAGCACAATCCACATTTGTGATGAGACCTCTGTCAGTGT 780
DB 721 CCTTATGGTGAATCCCGGTAGCACAATCCACATTTGTGATGAGACCTCTGTCAGTGT 780
QY 781 AGAATACAGTCACTGACTCCACTTCGTCAGCTGAGCGAGGAGGTTGCAAGTGCATTGC 840
DB 735 -----CTTGTGAGCGAGGAGGTTGCAAGTGCATTGC 767
QY 841 GGAATCTCCCGGTATGGTCTCAGCTGATGAAGAGTATAGCCTTGAAGACCCCAAGC 900
DB 768 GGAATCTCCCGGTATGGTCTCAGCTGATGAAGAGGATAGCCTTGAAGACCTCAAGC 827
QY 901 GAGCCCTCAGGCGAGCGGCTCGACAGTGTGAGCTTCGCGCACTACTGTGAGAGGACT 960
DB 828 GAGCCCTCAGGCGAGCGGCTCGACAGTGTGAGCTTCGCGCACTACTGTGAGAGGACT 887
QY 961 AAATTTGCTGCTGTTCTCAGCTGGCAAAACAGATCACAGCGCTCTGCTCGGTGTGGA 1020
DB 888 AAATTTGCTGCTGTTCTCGGCGTAGCAAAACAGATCACAGCGCTCTGCTCGGTGTGGA 947
QY 1021 AGCCACAGATCAGATGCTTTTCTCACCGACTACATCAAGAGTGCACCGGTCTCAG 1080
DB 948 AGCCACAGATCAGATGCTTTTCTCACCGACTACATCAAGAGTGCACCGGTCTCAG 1007

QY 1081 TAATATTCTCTCGACAAAGAGACGGCGGCACTATATGATGCAAAACAGGTGCGTG 1140
DB 1008 TAATATTCTCTCGACAAAGAGACGGCGGCACTATATGATGCAAAACAGGTGCGTG 1057
QY 1141 CGGTGCTCTCAGGTAGGGACTCGTTCCTTAGTGTCTATCCAGTATGCAAGTTCGATT 1200
DB 1058 -----CAGGTATGCAAGTTCGATT 1074
QY 1201 TGCCATGCCATGTCAAAAGGAACTTGTTCAGGCTCAGTGCACCTCAACACCCCGTGCCT 1260
DB 1075 TGCCATGCCATGTCAAAAGGAACTTGTTCAGGCTCAGTGCACCTCAACACCCCGTGCCT 1134
QY 1261 GGAATTGAGCAGTGGCGCTCGGCTGTATAGTACGATCGGCTCGGCGCGCTGTTCCGA 1320
DB 1135 GGAATTGAGCAGTGGCGCTCGGCTGTACAGTACGATCGGCTCGGCGCGCTGTTCCGA 1194
QY 1321 AGCAAAAGGTGGTTCGTTTACCAGACAATGTATCCACCTTTGACATTTTACCA 1380
DB 1195 AGCAAAAGGTGGTTCGTTTACCAGACAATGTATCCACCTTTGACATTTTACCA 1254
QY 1381 CCTCTTCCCGCGAGAAAGCAAGCATTCGCGGAAAAATCTATCCTCGGCTACTATGCAAG 1440
DB 1355 CCTCTTCCCGCGAGAAAGCAAGCATTCGCGGAAAAATCTATCCTCGGCTACTATGCAAG 1314
QY 1441 ATAGTCTTCGTATGGGACAAACCCGCTGTGCGGCAACAAGGCTTCTCGGCGCTCTCCAA 1500
DB 1315 ATAGTCTTCGTATGGGACAAACCCGCTGTGCGGCAACAAGGCTTCTCGGCGCTCTCCAA 1374
QY 1501 TCGAGCTGTGACCCCATCTCATTTGCCAGAGATACAGCATCGAAGTCGATCGGCAATGG 1560
DB 1375 TCGAGCTGTGACCCCATCTCATTTGCCAGAGATACAGCATCGAAGTCGATCGAATGG 1434
QY 1561 TCCATTACCTGTTTCATGTCGGAGACCCGGGACGGAAGTGTCCCAACAGTCCAAAGCAG 1620
DB 1435 TCCATTACCTGTTTCATGTCGGAGACCCGGGACGGAAGTGTCCCAACAGTCCAAAGCAG 1494
QY 1621 GTACGACAAAGTCTGTCTGGACCAACTCCGCGAGCCTACGAGAACGCCGGGCCCCAA 1680
DB 1495 GTACGACAAAGTCTGTCTGGACCAACTCCGCGAGCCTACGAGAACGCCGGGCCCCAA 1554
QY 1681 GTCCACAGACCGGCAACGCTCGTGAATCGAGTGTGCGAAGCAGCATTTTCCAAAGGA 1740
DB 1555 GTCCACAGACCGGCAACGCTCGTGAATCGAGTGTGCGAAGCAGCATTTTCCAAAGGA 1614
QY 1741 GCTCCGAGCGCGCTCTATGGGCTGAACGATCTCATACACTGGGTCGGCGCTCAGAAGC 1800
DB 1615 GCTCCGAGCGCGCTCTATGGGCTGAACGATCTCATACACTGGGTCGGCGCTCAGAAGC 1674
QY 1801 CCGTTCAAGTGTGTTTCATTTCTGTTGGAACGGAGACGCTTTTGTGGAAGGTTATG 1860
DB 1675 CCGTTCAAGTGTGTTTCATTTCTGTTGGAACGGAGACGCTTTTGTGGAAGGTTATG 1734
QY 1861 GAAGGGCCATACGATCGGCTCAACGAGGTGCTGCAAGTTCGTGCTAGCCTGGTGCCA 1920
DB 1735 GAAGGGCCATACGATCGGCTCAACGAGGTGCTGCAAGTTCGTGCTAGCCTGGTGCCA 1794
QY 1921 GCAGCATAG 1929
DB 1795 GCAGCATAG 1803

RESULT 9

AAZ58407

ID AAZ58407 standard; cDNA; 2490 BP.

XX AAZ58407;

AC

XX

DT 23-MAY-2000 (first entry)

XX

DNA encoding GST-truncated amino polyol amine oxidase fusion.

DE

XX Amino polyol amine oxidase; APO; fumonisin; mycotoxin;

KW transgenic plant; detoxification; animal feed; silage;

KW

selectable marker; glutathione S transferase; GST; mutant; ss.

Chimeric - Schistosoma japonicum.
Chimeric - Exophiala spinifera.
Synthetic.

Key Location/Qualifiers

sig_peptide 1..687
/tag= a
/product= "gst fusion + polylinker"

mat_peptide 688..2076
/tag= b

misc_feature 688..690
/product= "K:trAPAO"

mutation /tag= c
/note= "extra lysine"

mutation replace(1288..1290, TCC)

mutation /tag= d

mutation replace(1303..1305, AAC)

mutation /tag= e

W0200004159-Al.

27-JAN-2000.

08-JUL-1999; 99WO-US15454.

15-JUL-1998; 98US-0092936.

21-MAY-1999; 99US-0135391.

(PION-) PIONEER HI-BRED INT INC.

(CURA-) CURAGEN CORP.

Duwick JP, Gilliam JT, Maddox JR;

WPI; 2000-182425/16.

P-PSDB; AAY58918.

New isolated polynucleotides, polypeptides useful for detecting and degrading fumonisin or structurally related mycotoxin in processed grain or in silage -
Example 15; Page 131-135; 154pp; English.
The present sequence is that of a polynucleotide encoding a GST:APAO fusion protein (see AAY58918) composed of glutathione S transferase and Exophiala spinifera amino polyol amine oxidase (APAO). 2 Codons of the APAO coding region have been altered by site-directed mutagenesis in order to change the glycosylation pattern of the fusion protein. These were the replacement of AAT (Asn) by TCC (Ser) at codon 430, and replacement of AGC (Ser) by AAC (Asn) at codon 435. APAO is capable of degrading fumonisin and related mycotoxins. The invention provides APAO polynucleotides (see AAY58383-87) and polypeptides (see AAY58900-05) of E. spinifera and Rhinocladiella atrovirens. The polynucleotides are used to transform plant cells normally susceptible to Fusarium or other toxin-producing fungus infection. Also provided are methods for expressing APAO in transgenic plants, prokaryotic and non-plant eukaryotic systems. Methods for detoxification of grain, grain processing, silage, food crops and in animal feed and rumen microorganisms are also disclosed.

Sequence 2490 BP; 625 A; 623 C; 653 G; 589 T; 0 other;

Query Match 82.7%; Score 1596.2; DB 21; Length 2490;
Best Local Similarity 91.5%; Pred. No. 0;
Matches 1765; Conservative 0; Mismatches 38; Indels 126; Gaps 2;

QY 1 ATGGGCACTTGCACCGAGCTACATCAATCCCCAAACGTCGCTCCCCAGAGGGTATTCC 60

Db 688 ATGGGCACTTGCACCGAGCTACATCAATCCCCAAACGTCGCTCCCCAGAGGGTATTCT 747

QY 61 CACATCGGGCGTAGGGCCCAACGAAGCGAGGTATGTGACAATAGCTGGACAGATTGGACAA 120

Db 748 CACGTCGGCGTAGGCCAGAGCGAGGGAGGTATGTGCAATAGCTGGACAGATTGGACAA 807
QY 121 GACGCTTTGGGGGTGACAGACCCAGCCTACGAGAAACAGGTTGCCCAAGCAATTGCCCAAT 180
Db 808 GACGCTTCGGGGGTGACAGACCCCTCCCTACGAGAAACAGGTTGCCCAAGCAATTGCCCAAT 867
QY 181 CTGCGAGCTTGCTTGCCTTGCAGTTGGAGCCTCTTCAAAACGACGTCACCAAGCTCAATTAC 240
Db 868 CTGCGAGCTTGCTTGCCTTGCAGTTGGAGCCTCTTCAAAACGACGTCACCAAGCTCAATTAC 927
QY 241 TACATCGTCGACTACGCCGCCGAGCAAACTCACGCCAATTGGAGATGGGCTGAAGTCTACC 300
Db 928 TACATCGTCGACTACGCCGCCGAGCAAACTCACGCCAATTGGAGATGGGCTGAAGTCTACC 987
QY 301 TTTGCCCTTGACAGGTCCTCTTGCAGCTGGTGGCCAGTACCGGCTTGGCTTTCACCT 360
Db 988 TTTGCCCTTGACAGGTCCTCTTGCAGCTGGTGGCCAGTACCGGCTTGGCTTTCACCT 1047
QY 361 GAATACCTCTTTGAGTTGATGCCACGGGCTGGTGGCCAGGACACTCGACCCGACACAAAC 420
Db 1048 GAATACCTCTTTGAGTTGATGCCACGGGCTGGTGGCCGAGACACAGCACCCGACAAAC 1107
QY 421 GTTGGGACCTGGTGTGTGGGGCGCTGGCTTGGAGCGGTTTGGAGACGSCACGCAAAAGTC 480
Db 1108 GTTGGGACCTGGTGTGTGGGGCGCTGGCTTGGAGCGGTTTGGAGACGSCACGCAAAAGTC 1167
QY 481 CAGGCCCGCGGCTGTCTTCTTGGAGCGATGGATCGTGTAGGGGGAAGACT 540
Db 1168 CAGGCCCGCGGCTGTCTTCTTGGAGCGATGGATCGTGTAGGGGGAAGACT 1227
QY 541 CTGAGCGGTACAAATCGGGTCCCGCAGGAGGACTATCAACAGACTCGGCGCTCGCTGGATC 600
Db 1228 CTGAGCGGTACAAATCGGGTCCCGCAGGAGGACTATCAACAGACTCGGCGCTCGCTGGATC 1287
QY 601 AATGACAGCAACAAAGCAAGTATCCAGTGTGTTGAAAGATTTTCATTGAGGGGCGAG 660
Db 1288 TCCGACAGCAACAAAGCAAGTATCCAGTGTGTTGAAAGATTTTCATTGAGGGGCGAG 1347
QY 661 CTCACAGGACGACCGGAAATTCATCCATCAAGCAACAGAGCGGTACACCACTACAGCT 720
Db 1348 CTCACAGGACGACCGGAAATTCATCCATCAAGCAACAGAGCGGTACACCACTACAGCT 1407
QY 721 CCTATTGGTGACTCCCGGCTAAGCAACATCCACACTTTGTGTATGAGACCTCTGTGAGTGT 780
Db 1408 CCTATTGGTGACTC----- 1421
QY 781 AGAATACAGTCACTGACTCCACTTCGTCAGCTGACGAGGAGGTTGCAAGTGCACCTTGC 840
Db 1422 -----CTTGCTGAGCGAGGAGGTTGCAAGTGCACCTTGC 1454
QY 841 GGAACCTCTCCCGTATGGTCTCAGCTGATCGAAGAGATATAGCCTTTGAAGACCCCAAGGC 900
Db 1455 GGAACCTCTCCCGTATGGTCTCAGCTGATCGAAGAGATATAGCCTTCAAGACCTCAAGGC 1514
QY 901 GAGCCCTCAGCGAAGCGGCTGCACAGTGTGAGCTTCGCGCACTACTGTGAGAAGGACCT 960
Db 1515 GAGCCCTCAGCGAAGCGGCTGCACAGTGTGAGCTTCGCGCACTACTGTGAGAAGGAACT 1574
QY 961 AAACCTTGCCTGTCTTCTAGCGTGGCAACACAGATCACACGGCTCTGCTCGGTGTGGA 1020
Db 1575 AAACCTTGCCTGTCTTCTAGCGTGGCAACACAGATCACACGGCTCTGCTCGGTGTGGA 1634
QY 1021 AGCCACGAGATCAGCATGCTTTTCTCACCAGTACTATCAAGAGTGCACCGGCTCTCAG 1080
Db 1635 AGCCACGAGATCAGCATGCTTTTCTCACCAGTACTATCAAGAGTGCACCGGCTCTCAG 1694
QY 1081 TAATATTGTCTCGGACAAGAAAGACGGCGGCGAGTATATCGGATGCAAAACAGAGTGGTG 1140
Db 1695 TAATATTGTCTCGGACAAGAAAGACGGCGGCGAGTATATCGGATGCAAAA----- 1744
QY 1141 CGGTGTCTCTCAGGTAGGGGACTCGTTTCTTAGTGTCTATCCAGGTATGCAATCGATT 1200


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QY 241 TACATCGTCGACTAGCCGCCAGCAAACTCACCGCAATTGGAGATGGCTGAAGTCTACC 300
DB 928 TACATCGTCGACTAGCCGCCAGCAAACTCACCGCAATTGGAGATGGCTGAAGTCTACC 987
QY 301 TTGCGCCTTGACAGGCTCCCTCCTTGCACAGTGGTGCCAGTACCGGCTTGGCTTCACT 360
DB 988 TTGCGCCTTGACAGGCTCCCTCCTTGCACAGTGGTGCCAGTGGCTGGCTTGTCTCACT 1047
QY 361 GAATACCTCTTTGAGGTGATGCCACGGCGTGGTGCCAGAGCACTCGACCCAGACAAC 420
DB 1048 GAATACCTCTTTGAGGTGATGCCACGGCGTGGTGCCAGAGCACTCGACCCAGACAAC 1107
QY 421 GTTGGGAGCTGGTAGTGGTGGCGCTGGCTTGGAGCGTGGTGAGACGGCAGCAAAAGTC 480
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QY 601 AATGACAGCAACCAAGCGAAGTATCCAGATTGTTTGAAGATTTCATTTGGAGGGCGAG 660
DB 1288 TCCGACAGCAACCAAGCGAAGTATCCAGATTGTTTGAAGATTTCATTTGGAGGGCGAG 1347
QY 661 CTCAGAGGACGACCGGAAATTCATTCATCAAGCACAAGACGGTACAAACACTACAGCT 720
DB 1348 CTCAGAGGACGACCGGAAATTCATTCATCAAGCACAAGACGGTACAAACACTACAGCT 1407
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DB 1408 CTTTATGGTGACTC----- 1421
QY 781 AGAATACAGTCACTGACTCCACTTCGTCCTCCAGCTGAGCGAGGAGTTGCAAGTGCATTGC 840
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QY 841 GGAACCTCTCCCGTATGGTCTCAGCTCATGCAAGAGTATAGCCTTGAAGACCCCAAGGC 900
DB 1455 GGAACCTCTCCCGTATGGTCTCAGCTCATGCAAGAGTATAGCCTTGAAGACCTTCAAGGC 1514
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DB 1515 GAGCCTCAGGCGAAGCGGCTCGACAGTGTGAGCTTCGCGCACTACTGTGAGAAGGACT 1574
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QY 1141 CGGTGCTCTCAGTAGGGGACTCGTTTCTTAGTGTGCTATCCAGGTATGATCGATG 1200
DB 1745 -----CAGGTATGATCGATG 1761
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DB 2362 CCCTTCAAGTGTCTCATTTTCGTTGGAACGAGACGCTCTTTAGTTTGGAAAGGTTATATG 2421
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DB 2422 GAAGGGCCATACGATCGGCTCAACGAGGTGCTGCAAGAGTGTGCTGCTAGCCTGCTGCCA 2481
QY 1921 GCAGCATAG 1929
DB 2482 GCAGCATAG 2490
RESULT 11
AAZ58393
ID AAZ58393 standard; cDNA; 1442 bp.
XX
AC AAZ58393;
XX
DT 23-MAY-2000 (first entry)
XX
DE Amino polyol amine oxidase truncated DNA k0n0-395_5.4.
XX
KW Amino polyol amine oxidase; fumonisin; mycotoxin; transgenic plant;
KW detoxification; animal feed; silage; selectable marker; ss.
XX
OS Exophiala spinifera.
XX
FH Key Location/Qualifiers
FT CDS 1..1442
FT FT /*tag= a
FT FT /note= "contains an intron"
FT FT 647..699
FT FT /*tag= b
XX
PN WO200004159-A1.
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PF 08-JUL-1999; 99WO-US15454.
XX
PR 15-JUL-1998; 98US-0092936.
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XX AAZ60631;
XX 16-MAY-2000 (first entry)
XX
XX DNA encoding an aminopolyol amine oxidase clone trAPAO-I.
XX
XX Aminopolyol amine oxidase; APAO; mycotoxin degradation; antimicrobial;
XX plant fungal invasion; hydrogen peroxide; Fusarium; fungi; ss.
XX
XX Exophiala spinifera.
XX
XX Key Location/Qualifiers
XX CDS 1..1442
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XX 27-JAN-2000.
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XX 08-JUL-1999; 99WO-US15455.
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XX 15-JUL-1998; 98US-0092936.
XX
XX (PTON-) PIONEER HI-BRED INT INC.
XX (CURA-) CURAGEN CORP.
XX
XX Crasta OR, Duvick J, Folkerts O, Gilliam JT, Maddox JR;
XX
XX WPI: 2000-182426/16.
XX P-PSDB; RAY68844.
XX
XX New nucleic acid encoding aminopolyol amine oxidase, used, e.g. to
XX generate plants resistant to Fusarium -
XX
XX Example 6; Page 78-80; 145pp; English.
XX
XX The present sequence encodes an Exophiala spinifera aminopolyol amine
XX oxidase (APAO). The enzyme has homology to the flavin containing amine
XX oxidase family, that oxidise primary amine to an aldehyde or ketone,
XX releasing ammonia and hydrogen peroxide. The APAO enzyme degrades
XX mycotoxins that promote fungal invasion of plants. Destruction of
XX mycotoxins by APAO generates, as a by-product, hydrogen peroxide which
XX is itself an antimicrobial and stimulates the plants own defensive
XX systems. The APAO polynucleotides are used to generate plants
XX (particularly maize) that are resistant to Fusarium or other fungi
XX that produce mycotoxins and/or to degrade such mycotoxins (e.g. during
XX ensilaging); for recombinant production of APAO polypeptides; as
XX selection markers for plant transformation; and to isolate related
XX sequences from other organisms. The APAO polypeptides are used to
XX degrade mycotoxins in plant materials, including expression in
XX engineered bacteria and fungi, e.g. rumen microflora.
XX
XX Sequence 1442 BP; 336 A; 381 C; 416 G; 309 T; 0 other;
XX
XX Query Match 68.4%; Score 1319; DB 21; Length 1442;
XX Best Local Similarity 93.5%; Pred. No. 0;
XX Matches 1417; Conservative 0; Mismatches 25; Indels 73; Gaps 1;
XX
XX 415 GACAACGTTGGGACGTTGGTAGTGGTGGCGCTGGCTTGGAGCGGTTGGAGCGGCACGC 474
XX |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX 1 GACAACGTTGGGACGTTGGTAGTGGTGGCGCTGGCTTGGAGCGGTTGGAGCGGCACGC 60
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DB 301 ACAGCTCCTTATGCTGACTC-----CTTGCTGAGCGAGGAGTTTCAAGACCT 320
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QY 775 GAGTGTAGAATACAGTCACTGACTCCACTTCGTTCCAGCTGAGCGAGGAGTTTCAAGTGC 834
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DB 321 -----CTTGCTGAGCGAGGAGTTTCAAGTGC 347
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QY 835 ACTTGGGAACTCCTCCCGTATGCTGCTCAGGTGATGAAGATATAGCCTTTGAAGACC 894
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DB 588 TCTCAGTAATATGCTCTCGGACAAGAACGCGCGGAGTATATGCGATGCAAAACAGG 647
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DB 648 TGGTCCGCTGCTCTCAGGTAGGGGACTCGTTTCTTATGCTGCTATTCAGGTATGCGAG 707
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Db 2169 CACCGGTCTCAGTAATATGTCGCGACAAGAAAGAGCGCGGCAGTATATGCGATGCAA 2228
Qy 1129 AACAGGTGCGTGGGTCTCTCTCAGTAGGGGACTCGTTTCTTAGTGGTCATTCAGGT 1188
Db 2229 AA-----CAGGT 2235
Qy 1189 ATGAGTCGATTTGCCATGCCATGTCAAAGGAACCTTTTCCAGGCTCAGTGCACCTCAAC 1248
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Qy 1549 GATCGCAATGGTCCATTACCTGTTTCATGTCGGAGACCCGGGACCGGAAAGTGTGCCAA 1608
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Qy 1909 AGCGTGGTCCAGCAGCATAG 1929
Db 2956 AGCGTGGTCCAGCAGCATAG 2976
RESULT 14
AAZ60643
ID AAZ60643 standard; DNA; 2976 BP.
XX AAZ60643;
AC AAZ60643;
XX
DT 16-MAY-2000 (first entry)
XX
DE DNA encoding a fusion of aminopolylol amine oxidase/fumonisin esterase.

XX Aminopolylol amine oxidase; APAO; mycotoxin degradation; antimicrobial;
KW plant; fungal invasion; hydrogen peroxide; Fusarium; fungi;
KW fumonisin esterase; ss.
XX Synthetic.
OS Exophiala spinifera.
XX
FH Key Location/Qualifiers
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FT esterase fusion"
FT sig_peptide 1..72
FT /*tag= b
FT /note= "barley alpha amylase signal sequence"
FT 73..1545
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FT /product= "aminopolylol amine oxidase"
FT /note= "the protein has an amino terminal Lys
FT for optimized expression"
XX WO200004160-A1.
XX 27-JAN-2000.
XX 08-JUL-1999; 99WO-US15455.
XX 15-JUL-1998; 98US-0092936.
XX (PION-) PIONEER HI-BRED INT INC.
XX (CURA-) CURAGEN CORP.
XX Crasta OR, Duvick J, Folkerts O, Gilliam JT, Maddox JR;
XX WPI; 2000-182426/16.
XX P-PSDB; AAY68851.
XX New nucleic acid encoding aminopolylol amine oxidase, used, e.g. to
XX generate plants resistant to Fusarium -
XX Claim 14; Page 103-108; 145pp; English.
XX The present sequence encodes a fusion protein of Exophiala spinifera
XX aminopolylol amine oxidase (APAO) and a bacterial fumonisin esterase.
XX The APAO enzyme has homology to the flavin containing amine oxidase
XX family, that oxidise primary amine to an aldehyde or ketone, releasing
XX ammonia and hydrogen peroxide. The APAO enzyme degrades mycotoxins
XX that promote fungal invasion of plants. Destruction of mycotoxins by
XX APAO generates, as a by-product, hydrogen peroxide which is itself an
XX antimicrobial and stimulates the plants own defensive systems. The
XX APAO polynucleotides are used to generate plants (particularly maize)
XX that are resistant to Fusarium or other fungi that produce mycotoxins
XX and/or to degrade such mycotoxins (e.g. during ensiling); for
XX recombinant production of APAO polypeptides; as selection markers for
XX plant transformation; and to isolate related sequences from other
XX organisms. The APAO polypeptides are used to degrade mycotoxins in
XX plant materials, including expression in engineered bacteria and fungi,
XX e.g. rumen microflora.
XX
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Query Match 62.8%; Score 1212.2; DB 21; Length 2976;
Best Local Similarity 90.2%; Pred. No. 0;
Matches 1372; Conservative 0; Mismatches 23; Indels 126; Gaps 2;

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model
Run on: November 12, 2002, 02:21:50 ; Search time 2809 seconds
(without alignments)
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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| C 31 | 56.6 | 2.9 | 699 13 | BJ434208 |
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| C 34 | 55 | 2.9 | 639 9 | AU034174 |
| C 35 | 50.4 | 2.6 | 278 13 | BJ430253 |
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| C 43 | 46.4 | 2.4 | 588 13 | BJ434223 |
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| C 45 | 46.4 | 2.4 | 737 13 | BJ376587 |

ALIGNMENTS

RESULT 1
LOCUS BJ375584/C
DEFINITION BJ375584 Dictyostelium ddc19a09 3', mRNA sequence.
ACCESSION BJ375584
VERSION BJ375584.1 GI:19284967
KEYWORDS EST.
SOURCE Dictyostelium discoideum.
ORGANISM Dictyostelium discoideum
REFERENCE 1 (bases 1 to 729)
AUTHORS Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
TITLE Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
stage Full length cDNA of Dictyostelium discoideum at the culmination
Unpublished (2002)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
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/organism="Dictyostelium discoideum"
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ORIGIN
Query Match 3.0%; Score 58.8; DB 13; Length 729;
Best Local Similarity 44.3%; Pred. No. 1.5e-05;
Matches 295; Conservative 0; Mismatches 362; Indels 9; Gaps 1;
QY 1244 TCAACACCCCGCTGCGTGAATAGCAGTCGGCGTCCGGCTGTATAGTACGATCGGCT 1303
Db 712 TAAATGCACAGGCGCTTCATATTTCAGATGCCAATCAATGACCAATTAACACTGATA 653
QY 1304 CGGGCCCGCTGTTCCGAAGCAAAAGGTGGTGTTCGTTACCGACAACATTTATCCCA 1363
Db 652 ACGGTTCAACTTATCGTTCAAAATACATGTTGTTGCAATTCACCAACATTTGGCTGGCC 593
QY 1364 CTTTGACATTTTCACCACTCTTCCCGCGGAGAGCAAGCATTTGGCGGAAATCTATCC 1423
Db 592 GTATTCAATTATCAACATCTATGCCACCAAGACGTGATGAACCTCACTCAAGAATGCCAA 533
QY 1424 TCGGCTACTATAGCAAGATGCTTCGTATGGACAACCCGCTGGTGGCGGAACAAGCT 1483
Db 532 TGGTTCGCTCATTAACCACTACCACTATGATGAACCACTTCGGAGAAAGAGGTT 473
QY 1484 TPCGGGCGCTCCCAATCGAGTGTGACCCCATCTCATTTGCCAGAGATACCAATCG 1543
Db 472 ATTCACTGAAGCCATCTCTGATAAAGGTCCAACTCTTTATCTGCTATGATGACTCTTCC 413
QY 1544 AGTCATCGGCAATGTCATTAACCTGTTTCATGTCGGAGACCCGGAGGAGTGGT 1603
Db 412 ATGACGATGAAGAACAGCATTTGTTGGTTTCATTTGCTGCTTCAGCCGCTAAAGATTGG 353
QY 1604 CCCACAGTCCAAAGAGGTACGACAAAAGTCTGCTGGGACCAACTCCGCGCAGCTACG 1663
Db 352 CTGAAAAATCACCAGAGAAAGAGAGAGCGCTCTAGACTGTTATGCTGTTGGTGG 293
QY 1664 AGAACCCGGGCGCAAGTCCAGAGCCGCGCAACGTGCTCGAAATCGAGTGGTGAAGC 1723
Db 292 -----GTCCAAAGCAATTTATCTCCAAAGAACTCTTTTAGAGAAAAGTTGGAAGAAG 242
QY 1724 AGCAGTATTTCAAGAGCTCCGAGCGCGCTATATGGCTGAACCATCTCATCACTGG 1783
Db 241 AGAATATTCAGTGGTGTATTATAGTTACACTAGTCCAGGTACTCTACCAATGTG 182
QY 1784 GTCCGCGCTCAGAACCGGTTCAAGTGTGTTTCATTTGTTGGAACGGAGCGTCTTTAG 1843
Db 181 GTGAACATTTACGTGCTCCAGTTGGTAGAATTCATTTGGCTGGTGGTACAGAACTGCTTCAG 122
QY 1844 TTTGGAAAGGTATATGGAAGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAAGTTG 1903
Db 121 TTTGGATTGGTTATATGGAAGGTGCTTAGAATCAGGTTTATAGATTTCAAAGAAATTA 62
QY 1904 TGGCTA 1909
Db 61 AAGATA 56
RESULT 2
LOCUS BJ341279/c
DEFINITION BJ341279 Dictyostelium discoideum cDNA library, AF Dictyostelium
discoideum cDNA clone dda6b01 3', mRNA sequence.
ACCESSION BJ341279
VERSION BJ341279.1 GI:19249641
KEYWORDS EST.
SOURCE Dictyostelium discoideum.
ORGANISM Dictyostelium discoideum.
REFERENCE Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
AUTHORS 1 (bases 1 to 742)
Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
TITLE Full length cDNA of Dictyostelium discoideum at the aggregation
```

```
stage
Unpublished (2002)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
FEATURES
source
1. 742
/organism="Dictyostelium discoideum"
/strain="AX4"
/db_xref="taxon:44689"
/clone="dda6b01"
/clone_lib="Dictyostelium discoideum cDNA library, AF"
/sex="mat A"
/dev_stage="Aggregation stage"
BASE COUNT 215 a 142 c 132 g 252 t 1 others
ORIGIN
Query Match 3.0%; Score 58.8; DB 13; Length 742;
Best Local Similarity 44.3%; Pred. No. 1.5e-05;
Matches 295; Conservative 0; Mismatches 362; Indels 9; Gaps 1;
QY 1244 TCAACACCCCGCTGCGTGAATAGCAGTCGGCGTCCGGCTGTATAGTACGATCGGCT 1303
Db 706 TAAATGCACAGGCGTTCATATTTCAGATGCCAATCAATGTACCAATTAACACTGATA 647
QY 1304 CGGGCCCGCTGTTCCGAAGCAAAAGGTGGTGTTCGTTACCGACAACATTTATCCCA 1363
Db 646 ACGGTTCAACTTATCGTTCAAAATACATTTGTTGCAATTCACCAACATTTGGCTGGCC 587
QY 1364 CTTTGACATTTTCACCACTCTTCCCGCGGAGAGCAAGCATTTGGCGGAAATCTATCC 1423
Db 586 GTATTCAATTATCAACATCTATGCCACCAAGACGTGATGAACCTCACTCAAGAATGCCAA 527
QY 1424 TCGGCTACTATAGCAAGATAGTCTTCGTATGGACAACCCGCTGGTGGCGGAACAAGCT 1483
Db 526 TGGGTTCCGTCATTTAAACCATCACCATCTAGATGAACCATTTCTGGAGAAAAGAGTT 467
QY 1484 TCTCGGCGCTCTCCCAATCGAGCTGTGACCCCATCTCATTTGCCAGAGATACCAATCG 1543
Db 466 ATTCACTGAAGCCATCTCTGATAAAGGTCCAACTCTTTATCTGCTATGACTCTTCAC 407
QY 1544 AAGTCGATCGGCAATGTCATTAACCTGTTTCATGTCGGAGACCCGGGACGGAAGTGT 1603
Db 406 ATGACGATAAGAAAACAGCTATCGTTGGTTTCATTCGCTTCAGCCGCTAAAGATTGG 347
QY 1604 CCCAACAGTCCAAAGCAGGTACGACAAAAGTCTCTCTGGGACCAACTCCGCGCAGCTAGG 1663
Db 346 CTGAAAAATCACCAGAGAAAGAAAGAGAGCCGCTCTTAGACTGTTATGCTGTTGGTGG 287
QY 1664 AGAACCCGGGCGGCAAGTCCCGAGCGGCGCAACGTGCTCGAAATCGAGTGGTGAAGC 1723
Db 286 -----GTCCAAAGCAATTTATCTCCAAAGAACTCTTTTAGAGAAAAGTTGGAAGAAG 236
QY 1724 AGCAGTATTTCCAAAGAGCTCCGAGCGCGCTATGCGTGAACGATCTCATCACTGG 1783
Db 235 AAGAATATTCAGTGGTGTATTATAGTTACACTAGTCCAGGTACTCTTACCAATGTG 176
QY 1784 GTTCGGCGCTCAGAACCGCGCTTCAAGTGTGTTTCATTTGTTGGAACGGAGAGCTTTTAG 1843
Db 175 GTGAACATTTACGTGCTCCAGTTGGTGAATTCATTTGGCTGGTACAGAACTGCTTCAG 116
QY 1844 TTTGGAAAGGTATATGGAAGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAAGTTG 1903
Db 115 TTTGGATTGGTTATATGGAAGGTGCGCTTAGAATCAGGTTTATAGAGTTTCAAAAGAAATTA 56
QY 1904 TGGCTA 1909
Db 55 AAGATA 50
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RESULT 3
BJ373006/c
LOCUS      BJ373006      711 bp      mRNA      linear      EST 08-MAR-2002
DEFINITION BJ373006 Dictyostelium discoideum cDNA library, CF Dictyostelium
            discoideum cDNA clone ddc15e09 3', mRNA sequence.
ACCESSION  BJ373006
VERSION     BJ373006.1  GI:19282389
KEYWORDS    EST.
SOURCE      Dictyostelium discoideum.
ORGANISM    Dictyostelium discoideum.
            Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
REFERENCE   1 (bases 1 to 711)
AUTHORS     Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
TITLE       Full length cDNA of Dictyostelium discoideum at the culmination
            stage
JOURNAL      Unpublished (2002)
COMMENT     Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp.
            Location/Qualifiers
FEATURES             source
BASE COUNT           219 a 130 c 121 g 240 t 1 others
ORIGIN
Query Match          3.0%; Score 57.8; DB 13; Length 711;
Best Local Similarity 45.1%; Pred. No. 2.8e-05;
Matches 264; Conservative 0; Mismatches 313; Indels 9; Gaps 1;
QY 1324 AAAAAGGTGGTTCGTTACCGACACATGATATCCACCTTGACATTTTCACCACT 1383
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Db 655 AAATACATTTGTTGCAATTCACCAACATTTGGTGGCGGTATTCATTTACCACTCT 596
QY 1384 CTTCCCGCGGAGAACGACATTCGGCGAAATATCTCTCGCTACTATAGCAAGATA 1443
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Db 595 ATGCCACCAAGACGTGATGAATCTACTCAAAGATGCCAATGGGTTCGTCATTAAACC 536
QY 1444 GTCTTCGTATGGGACACCGGTGGCGGACAAAGGCTTCTCGGGGGTCTCCCAATCG 1503
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Db 535 ATCACCATCTATGATGAACCATTTNCGGAGAAAGAGGTATTACGCTGAAGCCATCTCT 476
QY 1504 AGCTGTGACCCCATCTATTTGCCAGATACCAAGCATCGAAGTCGATCGCAATGFTCC 1563
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Db 475 GATAAAGGTCCAAATCTTTATCTGCTATGATGACTCTTCACATGACGATAAGAAACAGCT 416
QY 1564 ATTACCTGTTTCATGGTCGGACACCGCGGACGAGTGGTCCACACATCTCAAGCAGTA 1623
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Db 415 ATCGTGTGTTTCATTCGCTGCTTCAGCCGCTAAAGATTTGGGTGAAAAATACCCAGAGAA 356
QY 1624 CGACAAAAGCTCTGCTGGGACCAACTCCGCGCAGGCTACGAGAACGCGCGGCCCAAGTC 1683
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 355 AGAAGAGAGCCGCTTAGACTGTTATGCTCGTTGGT-----GGGTCCAAAGCA 305
QY 1684 CCAGAGCCGGCCAAAGTGCCTGAATTCGAGTGGTTCGAGACGACAGTATTTTCCAGGAGCT 1743
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Db 304 TTATCTCCAAAGAAATCTTTTAGAGAAAAGTTGGAAGAAGAGAATAATTACGCTGTTGT 245
QY 1744 CCGAGCCCGCTCTATGGGCTGAAACATCTCATCACACTGGGTTCGGCGCTCAGAACGCCG 1803
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Db 244 TATTTAGGTTACACTAGTCCAGGTACTCTCTACCAATTTGGTGAACATTTACGTCTCCA 185
QY 1804 TTCAAGTGTGTTCAATTCGTTGGAACGGAGACGTCCTTTTAGTTTGGAAAGGTATATGAA 1863
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Db 184 GTTGGTAGAATTCATTGGGCTGGTACAGAAACTGCTCAGTTTGGATTGTTATATATGAA 125
QY 1864 GGGGCCATCAGATCGGGTCAACAGAGTCTGCAGAAAGTTGTGGCTA 1909
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Db 124 GGTGCTTAGAATCAGGTTTGTAGAGTTTCAAAAGAAATTAAGATA 79
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RESULT 4
BJ377633/c
LOCUS      BJ377633      730 bp      mRNA      linear      EST 08-MAR-2002
DEFINITION BJ377633 Dictyostelium discoideum cDNA library, CF Dictyostelium
            discoideum cDNA clone ddc25101 3', mRNA sequence.
ACCESSION  BJ377633
VERSION     BJ377633.1  GI:19287016
KEYWORDS    EST.
SOURCE      Dictyostelium discoideum.
ORGANISM    Dictyostelium discoideum.
            Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
REFERENCE   1 (bases 1 to 730)
AUTHORS     Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
TITLE       Full length cDNA of Dictyostelium discoideum at the culmination
            stage
JOURNAL      Unpublished (2002)
COMMENT     Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp.
            Location/Qualifiers
FEATURES             source
BASE COUNT           211 a 141 c 130 g 243 t 5 others
ORIGIN
Query Match          3.0%; Score 57.4; DB 13; Length 730;
Best Local Similarity 44.9%; Pred. No. 3.7e-05;
Matches 263; Conservative 0; Mismatches 314; Indels 9; Gaps 1;
QY 1324 AAAAAGTGTGTTGTTTACCGACAAACATTTGATCCCACCTTGACATTTTCACCACT 1383
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Db 611 AAATACATTTGTTGCAATTCACCAACATTTGGCTGCGGTATTCATTTACCACTCT 552
QY 1384 CTTCCCGCGGAGAGCAAGCATTTGGGGGAAAAATCTATCCTCGGTACTATAGCAAGATA 1443
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Db 551 ATGCCACCAAGACGTGATGAACCTCACTCAAAGAATGCCAATGGGTTCGCTCAATAAAC 492
QY 1444 GTCTTCGTATGGGACACCGGTGGCGGACAGAGCTTCTCGGGCGTCCCTCAATCG 1503
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Db 491 ATCACCATCTATGATGAACCATTTCTGGAGAAAAGAGGTTATTTCAGCTGAAGCCATCTCT 432
QY 1504 AGCTGTGACCCCATCTCTCATTTGGCAGAGATACCAGCATCGAAGTCATCGCAATGGTCC 1563
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 431 GATAAAGGTCCATCTTTATCTGCTATGATGACTCTTCACATGACGATAGAAACAGCT 372
QY 1564 ATTACCTGTTTCATGTCGGAGACCGGGACGGGAAGTGGTCCCAAGCTCCAGCAGGTA 1623
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Db 371 ATCGTGTGTTTCATTCGCTGCTTCAGCGCTAAAGATTTGGGTGAAAAATACCCAGAGAA 312
QY 1624 CGACAAAAGCTCTCTCGGACCAACTCCGCGCAGCCTACGAGAACGCCGGGCCCCAAGTC 1683
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Db 311 AGAAGAGAGCCGCTCTTAGACTGTTATGCTCGTTGGT-----GGGTCCAAAGCA 261
QY 1684 CCAGAGCCGGCCAAAGCTGCTCGAAATCGAGTGGTTCGAAGCAGCAGTATTTTCCAGGAGCT 1743
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Db 260 TTATCTCCAGAAATCTTTTAGAGAAAAGTTGGAAGAAGAAGAAATATATTCACGTGGTTGT 201
QY 1744 CCGAGCGCGTCTATGGGTGAACGATCTCATCACATCGGTTCCGGCTCAGAACGCG 1803
Db 200 TATTTAGGTTACACTAGTCCAGGTACTCTCTACCACTGTGGTGAACATTNACGTCTCCA 141
QY 1804 TTCAGTGTGTTCAATTCGTTGGACGGAGAGCGTCTTAGTTTGGAAAGGATATATGAA 1863
Db 140 GTTGTGAGAAATTCATTTGGCTGCGACAGAACTGCTTCAGTTTGGATTGGTTATATGAA 81
QY 1864 GGGGCCATACGATCGGTCACAGGTCGTCGACAGTGTGCGCTA 1909
Db 80 GGTGCTTAGAATCAGGTTTGTAGAGTTTCAAAAGAAATTAAGATA 35

RESULT 5
BJ431313/c
LOCUS
DEFINITION
  BJ431313 Dictyostelium discoideum cDNA library, VF Dictyostelium
  discoideum cDNA clone dvl3p15 3', mRNA sequence.
ACCESSION
  BJ431313
VERSION
  BJ431313.1 GI:19406035
KEYWORDS
  EST.
SOURCE
  Dictyostelium discoideum.
  Dictyostelium discoideum.
  Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
REFERENCE
  1 (bases 1 to 610)
  Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-I,T.
  Full length cDNA of Dictyostelium discoideum at the vegetative
  stage
JOURNAL
  Unpublished (2002)
COMMENT
  Contact: Tadasu Shin-I
  Center For Genetic Resource Information
  National Institute of Genetics
  1111 Yata, Mishima, Shizuoka 411-8540, Japan
  Tel: 81-559-81-6856
  Fax: 81-559-81-6855
  Email: tshini@genes.nig.ac.jp.
  Location/Qualifiers
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      /organism="Dictyostelium discoideum"
      /strain="AX4"
      /db_xref="taxon:44689"
      /clone="dvl3p15"
      /clone_lib="Dictyostelium discoideum cDNA library, VF"
      /sex="mat A"
      /dev_stage="Growth phase"
      179 a 122 c 107 g 201 t 1 others

BASE COUNT
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ORIGIN

Query Match 3.0%; Score 57.2; DB 13; Length 610;
Best Local Similarity 45.1%; Pred. No. 3.8e-05;
Matches 261; Conservative 0; Mismatches 309; Indels 9; Gaps 1;

QY 1324 AAAAGGTGGTTCGTTACCGACACATGTATCCACCTTGACATTTTCACCACCT 1383
Db 610 AAATACATTTGTTGCAATTCACCAACATTCGCTGCNGTATTCATTTATTCACCATCT 551
QY 1384 CTTCCCGCGAGAACGACATTCGCGGAAAAATCTATCTCGGTACTATAGCAAGATA 1443
Db 550 ATGCCACCAAGACGTGATGACTCACTCAAGATGCCAATGGTTCGTCATTAATAACC 491
QY 1444 GTCTTCGATGGACAACCCGTTGGCGGCAACAGGCTTCCTCGGGCGTCCCTCAATCG 1503
Db 490 ATCACCATCTATGATGAACCATTCCTGGAAAAAGAGGTTATTTCAGCTGAAGCCATCTCT 431
QY 1504 AGCTGTGACCCCATCTCATTTGCCAGATATACCAGATCGAAGTCGATGGCATGGTCC 1563
Db 430 GATAAAGTCCCAATCTTTATCTGCTATGATGACTCTTCACATGACGATAAGAAAAACAGCT 371
QY 1564 ATTACCTGTTTCATCGTCGGAGACCCGGAGCGGAGTGGTCCCAACAGTCCCAAGCAGGTA 1623
Db 370 ATCGTGTGTTTCATCTGCTGCTTCAGCCCTTAAGATTGGGCTGAAAATCACCAGAAAG 311
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QY 1624 CGACAAAAGTCTGTCTGGGACCAACTCCGGCAGCCCTACGAGAACGCCGGGCCAAGTC 1683
Db 310 AGAAGAGAGCCGCTCTTAGACTGTTATGCTCGTTGGT-----GGGTCCAAAGCA 260
QY 1684 CCAGAGCCGGCCAAACGTCGCTCGAAATCGAGTGGTGAAGCAGCAGTAGTATTTCCAAGAGCT 1743
Db 259 TTATCTCCAAGAATCTTTTAGAGAAAAGTTGGAAGAAGAAGAAATATTCACGTGGTTGT 200
QY 1744 CCGAGCCCGCTCTATGGCTGAACGATCTCATCACACTGGTTCGGCGCTCACAACGCCG 1803
Db 199 TATTTAGGTTACACTAGTCCAGGTACTCTTACCAATGTGTGAACATTTACGTGCTCCA 140
QY 1804 TTCAAGTGTGTTTCATTTGTTGGAACGGAGACGCTCTTAGTTTGGAAAGGATATATGAA 1863
Db 139 GTTGTAGAATTCAATTGGCTGGTACAGAACTGCTTCAGTTTGGATTGGTTATATGAA 80
QY 1864 GGGGCCATACGATCGGTCACAGGTCGTCGACAGGTT 1902
Db 79 GGTGCTTAGAATCAGGTTTGTAGAGTTTCAAAAGAAAT 41

RESULT 6
BJ374786/c
LOCUS
DEFINITION
  BJ374786 Dictyostelium discoideum cDNA library, CF Dictyostelium
  discoideum cDNA clone ddc16d07 3', mRNA sequence.
ACCESSION
  BJ374786
VERSION
  BJ374786.1 GI:19284169
KEYWORDS
  EST.
SOURCE
  Dictyostelium discoideum.
  Dictyostelium discoideum.
  Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
REFERENCE
  1 (bases 1 to 611)
  Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-I,T.
  Full length cDNA of Dictyostelium discoideum at the culmination
  stage
JOURNAL
  Unpublished (2002)
COMMENT
  Contact: Tadasu Shin-I
  Center For Genetic Resource Information
  National Institute of Genetics
  1111 Yata, Mishima, Shizuoka 411-8540, Japan
  Tel: 81-559-81-6856
  Fax: 81-559-81-6855
  Email: tshini@genes.nig.ac.jp.
  Location/Qualifiers
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      /organism="Dictyostelium discoideum"
      /strain="AX4"
      /db_xref="taxon:44689"
      /clone="ddc16d07"
      /clone_lib="Dictyostelium discoideum cDNA library, CF"
      /sex="mat A"
      /dev_stage="Culmination stage"
      181 a 125 c 113 g 192 t

BASE COUNT
  181 a 125 c 113 g 192 t
ORIGIN

Query Match 3.0%; Score 57.2; DB 13; Length 611;
Best Local Similarity 45.1%; Pred. No. 3.8e-05;
Matches 264; Conservative 0; Mismatches 313; Indels 9; Gaps 1;

QY 1324 AAAAGGTGGTTCGTTACCGACACATTTGATCCACCTTGACATTTTCACCACCT 1383
Db 592 AAATACATTTGTTGCAATTCACCAACATTCGCTGGCGGTATTCATTTATTCACCATCT 533
QY 1384 CTTCCCGCGAGAACGACATTCGCGGAAAAATCTATCTCGGTACTATAGCAAGATA 1443
Db 532 ATGCCACCAAGACGTGATGAACCTCACTCAAGAAATGCCAATGGGTTCCGCTCAATAAAC 473
QY 1444 GTCTTCGATGGACAACCCGTTGGCGGCAACAGGCTTCCTCGGGCGTCCCTCAATCG 1503
Db 472 ATCACCATCTATGATGAACCATTCCTGGAAAAAGAGGTTATTTCAGCTGAAGCCATCTCT 413
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| QY | 1504 | AGCTGTGACCCATCTCATTTGCCAGAGATACACAGCATCGAAGTCCGCGAATGGTCC | 1563 |
|-----------------------|---|--|--------------------|
| Db | 412 | GATAAGGTCCAACTCTTTATCTGCTATGATGACTCTTTACATGACGATAAGAAACAGCT | 353 |
| QY | 1564 | ATTACCTGTTTCATGGTCGGAGACCGCGGAGGTGGTCCCAACAGTCCAAAGCAGGTA | 1623 |
| Db | 352 | ATCGTTGGTTTCATGCTGCTTACCGCTTAAGATTGGGCTGAAAATCACCAGAGAA | 293 |
| QY | 1624 | CGACAAAAGTCTGCTGGGCAACTCCGGCGACGCTACGAGAACGCGCGGCGCCAAAGTC | 1683 |
| Db | 292 | AGAAAGAGCGCTTAGACTGTTATGCTGTTGGT-----GGGTCCAAAAGCA | 242 |
| QY | 1684 | CCAGAGCGGCCACAGTGCTCGAAATCGATGGTGCAGAGCAGATGATTTCCAAAGGAGCT | 1743 |
| Db | 241 | TTATCTCAAGAATCTTTTATAGAAAAAGTTGGAAGAAGAAGAAATATTCACGTGGTTGT | 182 |
| QY | 1744 | CGAGCGCGTCTATGGGCTGAACGATCTCATCAGCTGGTTCGGCGCTCAGAACGCCG | 1803 |
| Db | 181 | TATTAGGTTACACTAGTCCAGGTACTCTACCAATGTGGTGAACATTTACGTGCTCCA | 122 |
| QY | 1804 | TTCAAGTGTGTTTCATTTTCGTTGGAACGGAGACGCTTTTAGTTTGGAAAGGTATATGAA | 1863 |
| Db | 121 | GTGGTAGAATTCATTTGGGCTGGTACAGAACTGCTTCAGTTGGATTTGTTATATGAA | 62 |
| QY | 1864 | GGGGCCATACATCGGTTCACAGAGGTGCTGCAGAGTTGTGGCTA | 1909 |
| Db | 61 | GGTGCTTAGAATCAGGTTTTAGAGTTTCAAAAGAAATTAAGATA | 16 |
| RESULT 7 | | | |
| BJ428963/c | | | |
| LOCUS | | | |
| DEFINITION | BJ428963 | Dictyostelium 612 bp mRNA linear EST 13-MAR-2002 | |
| ACCESSION | BJ428963 | Dictyostelium cDNA clone ddvj21 3', mRNA sequence. | |
| VERSION | BJ428963.1 | GI:19403685 | |
| KEYWORDS | Dictyostelium discoideum. | | |
| SOURCE | Dictyostelium discoideum. | | |
| ORGANISM | Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium. | | |
| REFERENCE | 1 (bases 1 to 612) | | |
| AUTHORS | Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T. | | |
| TITLE | Full length cDNA of Dictyostelium discoideum at the vegetative stage | | |
| JOURNAL | Unpublished (2002) | | |
| COMMENT | Contact: Tadasu Shin-i Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-6855 Email: tshini@genes.nig.ac.jp. | | |
| FEATURES | Location/Qualifiers | | |
| source | 1..612 /organism="Dictyostelium discoideum" /strain="AX4" /db_xref="taxon:44689" /clone="ddvj21" /clone_lib="Dictyostelium discoideum cDNA library, VF" /sex="mat A" /dev_stage="Growth phase" | | |
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| ORIGIN | | | |
| Query Match | 3.0%; | Score 57.2; | DB 13; Length 612; |
| Best Local Similarity | 45.1%; | Pred. No. 3.8e-05; | |
| Matches 264; | Conservative 0; | Mismatches 313; | Indels 9; Gaps 1; |
| QY | 1324 | AAAAAGGTGGTTCGTTTACCGACCAACATGTATCCACCTTGACATTTTCCACACT | 1383 |
| Db | 591 | AAATACATTTGTTGGCAATTCACCAACATTTGGCTGGCGGTATTCATTTACCATCT | 532 |
| QY | 1384 | CTTCCGCGCGAGAAGCAAGCATTTGGCGGAAAAATATCTCTCGGTACTATAGCAAGATA | 1443 |

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QY 1324 AAAAGTGGTGGTTCGTACCGACAACATGTTATCCACCTTGACATTTTCACCACT 1383
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Db 617 AAATACATTTGTTGCAATTCACCAACATTTGGTGGCGGTATTCATTTACCACTCT 558
QY 1384 CTTCCCGCGGAGAAGCATTTGGCGGAAATCTATCCTCGGTACTATAGCAAGATA 1443
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 557 ATGCCACCAAGACGTGATGAATCACTCAAGAATGCCAATGGGTTCGGTCAATTAAC 498
QY 1444 GTCTTCGTATGGACACCGGTGGCGGACAAGGCTTCTCGGGGTCTCCTCAATCG 1503
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Db 497 ATCACATCTATGATGAACCATTTGGAGAAAGAGGTATTTACAGCTGAAGCCATCTCT 438
QY 1504 AGCTGTGACCCCATCTCAATTTGCCAGATACCAAGCATCGAAGTCGGATGGTTC 1563
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Db 437 GATAAAGGTCCAACTTTATCTGCTATGATGACTCTTCACATGAGGATAAGAAACAGCT 378
QY 1564 ATTACCTGTTTCATGGTGGAGACCGGAGCGGAAGTGGTCCCAACAGTCAAGCAGTA 1623
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Db 377 ATCGTTGGTTTCATTTGCTGCTTACGCCCTAAAGATTGGGCTGAAATACACCAAGAA 318
QY 1624 CGACAAAAGTCTGTCTGGGACCAACTCCGCGCAGCTACGAGACGCGGGGCCCAAGTC 1683
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Db 317 AGAAGAGAGCGCTTTAGACTGTTATGCTGTTGCT-----GGGTCCAAAAGCA 267
QY 1684 CCAGAGCGGCGCAACGCTCGAATTCGAGTGGTGAAGCAGCAGTATTTCCAAAGGAGCT 1743
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Db 266 TTATCTCCAAGAATCTTTTAGAGAAAAGTTGGAAGAAGAATAATTCACGTTGGTGT 207
QY 1744 CCGAGCGCGTCTATGGCTGACAGCATCTACACACTGGGTTGGCGCTCAGAACGCG 1803
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Db 206 TATTTAGGTTACAGTAGTCCAGGTAATCTTACCAATGGTGGAACATTTACGTTGCCA 147
QY 1804 TTCAAGTGTGTTCAATTCGTTGAACGAGAGAGCTTTTAGTTTGAAGGTTATATGAA 1863
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Db 146 GTTGTAGAAATTCATTTGGCTGGTACAGAACTGCTTCAGTTTGGATTGGTTATATGAA 87
QY 1864 GGGGCCATACAGTCCGGTCAACGAGTGTCTGCAGAAGTTTGGGCTA 1909
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Db 86 GGTGCTTAGAATCAGGTTTATAGATTTTCAAAGAAGAAATTAAGATA 41

RESULT 9
BJ375424/c BJ375424 548 bp mRNA linear EST 08-MAR-2002
LOCUS BJ375424 Dictyostelium discoideum cDNA library, CF Dictyostelium
DEFINITION BJ375424
ACCESSION BJ375424.1 GI:19284807
VERSION EST.
KEYWORDS Dictyostelium discoideum.
SOURCE Dictyostelium discoideum.
ORGANISM Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.
REFERENCE 1 (bases 1 to 648)
AUTHORS Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
TITLE Full length cDNA of Dictyostelium discoideum at the culmination
stage
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-i
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
1. .648
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/strain="AX4"
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/clone="ddcl8m13"
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/sex="mat A"

FEATURES
source
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BASE COUNT 191 a 125 c 114 g 217 t 1 others
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Query Match 3.0%; Score 57.2; DB 13; Length 648;
Best Local Similarity 45.1%; Pred. No. 3.9e-05;
Matches 264; Conservative 0; Mismatches 313; Indels 9; Gaps 1;
QY 1324 AAAAGTGGTGGTTCGTACCGACAACATGTTATCCACCTTGACATTTTCACCACT 1383
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Db 626 AAATACATTTGTTGCAATTCACCAACATTTGGTGGCGGTATTCATTTACCACTCT 567
QY 1384 CTTCCCGCGGAGAAGCATTTGGCGGAAATCTATCCTCGGCTACTATACAGATA 1443
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Db 566 ATGCCACCAAGACGTGATGAATCTCAAGAATGCCAATGGGTTCGGTCAATTAAC 507
QY 1444 GTCTTCGTATGGACAAACCGGTGGCGGAAACAAAGGCTTCTCGGGCGCTCTCCAATCG 1503
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Db 506 ATCACATCTATGATGAACCATTTCTGAGAAAAGAGTTTATTCAGCTGAAGCCATCTCT 447
QY 1504 AGCTGTGACCCCATCTCAATTTGCCAGAGATACCAAGCATCGAAGTCGATCGCAATGGTCC 1563
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Db 446 GATAAAGGTCCAACTTTATCTGCTATGATGACTCTTCACATGACGATAAGAAACAGCT 387
QY 1564 ATTACCTGTTTCATGGTGGAGACCGCGGAGAACTGGTCCCAACAGTCCAAGCAGTA 1623
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Db 386 ATCGTTGGTTTCATTTGCTGCTTCAGCGCTAAAGATTGGCTGAAAATACCAAGAA 327
QY 1624 CGACAAAAGTCTGTCTGGGACCAACTCCGCGCAGCTACGAGAACCGCGGGCCCCAAGTC 1683
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Db 326 AGAAGAGAGCGCTCTTAGACTGTTATGCTGCTGCT-----GGGTCCAAAAGCA 276
QY 1684 CCAGAGCGGCGCAACGCTCGAATCGAGTGGTGTCAAGCAGCAGTATTTCCAAGGAGCT 1743
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Db 275 TTATCTCCAAGAATCTTTTAGAGAAAAGTTGGAAGAAGAAGATAATTCACGTTGGTGT 216
QY 1744 CCGAGCGCGCTCTATGGGCTGAACGATCTCATCACACTCGGTTCCGCGCTCAGAACGCG 1803
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Db 215 TATTTAGGTTACACTAGTCCAGGTACTCTCTACCAATGGTGAACATTTACGTGCTCA 156
QY 1804 TTCAAGTGTGTTCAATTCGTTGAACGAGAGAGCTCTTTAGTTTGAAGGTTATATGAA 1863
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Db 155 GTTGTAGAAATTCATTTGGGCTGTACAGAAACTGCTCAGTTTGGATTGGTTATATGAA 96
QY 1864 GGGGCCATACGATCGGTCGAACGAGTGTCTGCAGAAGTTTGTGCTA 1909
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Db 95 GGTGCTTAGAATCAGGTTTATAGATTTCAAAGAAGAAATTAAGATA 50

RESULT 10
BJ375565/c BJ375565 650 bp mRNA linear EST 08-MAR-2002
LOCUS BJ375565 Dictyostelium discoideum cDNA library, CF Dictyostelium
DEFINITION BJ375565
ACCESSION BJ375565
VERSION BJ375565.1 GI:19284948
KEYWORDS EST.
SOURCE Dictyostelium discoideum.
ORGANISM Dictyostelium discoideum.
REFERENCE 1 (bases 1 to 650)
AUTHORS Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
TITLE Full length cDNA of Dictyostelium discoideum at the culmination
stage
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
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FEATURES

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/organism="Dictyostelium discoideum"
/db_xref="AX4"
/strain="ddc19m05"
/clone_lib="Dictyostelium discoideum cdna library, CF"
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BASE COUNT 192 a 124 c 113 g 221 t
ORIGIN

Query Match 3.0%; Score 57.2; DB 13; Length 650;
Best Local Similarity 45.1%; Pred. No. 3.9e-05;
Matches 264; Conservative 0; Mismatches 313; Indels 9; Gaps 1;

Qy 1324 AAAAAGTGGTGGTTTCGTTACCGACAAATGTATCCCACTTGACATTTTCACCACT 1383
Db 633 AAATACATTTGTTGCAATTCACCAACATTTGGCTGGCGGTATTCATTTATCACCATCT 574

Qy 1384 CTTCCCGCGAGAACGATTCGGCGGAAAAATCTATCCTCGCTACTATAGCAAGATA 1443
Db 573 ATGCCACCAAGACGTGATGAATCCTCAAGAAATGCCAATGGTTCCGTCTATTAACCC 514

Qy 1444 GTCTTCGTATGGGACAAACCGTGGTGGCGGACAAAGCTTCTCGGCGTCTCCCAATCG 1503
Db 513 ATCACCATCTATGATGAACCATTTCTGGAGAAAGAGGTTATTTCAGCTGAAGCCATCTCT 454

Qy 1504 AGCTGTGACCCCATCTCATTTGCCAGAGATACCAAGTCGATCGCAATGGTCC 1563
Db 453 GATAAAGGTCCAAATCTTATCTGTATGATGACTCTTCACATGACGATAGAAACAGCT 394

Qy 1564 ATTACCTGTTTCATGTCGGAGACCGGAGGAGTGGTCCCAACAGTCCCAAGCAGGTA 1623
Db 393 ATCGTTGTTTCATGCTGCTTTCAGCCGCTTAAGATTTGGCTGAAATATCACCAGAGAA 334

Qy 1624 CGACAAAAGTCTGTCTGGGCAACTCCGCGCAGCCTACGAGAACGCCGGGCCCCAAGTC 1683
Db 333 AGAAAGAGAGCGCTTAGACTGTTATGCTCGTTGGT-----GGGGTCCAAAAGCA 283

Qy 1684 CCAGAGCGGCGCAAGCTGCTCAATCGATGGTCGAGCAGCAGTATTTCCAAAGGAGCT 1743
Db 282 TTATCTCCAAGAATCTTTTAGAGAAAAGTTGGAAGAAAGAAATATTCACGTGGTGT 223

Qy 1744 CCGAGCGCGTCTATGGGCTCAAGCATCTATCACACTGGTTCGGCGCTCAGAACCGCG 1803
Db 222 TATTAGTTTACACTAGTCCAGGTACTCTACCAATGTGTGACATTTACGTGCTCCA 163

Qy 1804 TTCAAGTGTGTTCAATTTGGTGGAAACGAGACGTCTTTAGTTTGGAAAGGTATATGGAA 1863
Db 162 GTTGGTAGAATTCATTTGGGCTGGTACAGAACTGCTTCAGTTTGGATTGGTTATATGGAA 103

Qy 1864 GGGGCCATACGATCGGTCACAGAGTCTGCAGAAAGTTGTGGCTA 1909
Db 102 GGTGCCCTTAGAATCAGGTTTATAGAGTTTCAAAAAGAAATTAAGATA 57

RESULT 11
BJ372067/c 651 bp mRNA linear EST 08-MAR-2002
LOCUS BJ372067 Dictyostelium discoideum cdna library, CF Dictyostelium
DEFINITION dictyostelium cdna clone ddc1k04 3', mRNA sequence.
ACCESSION BJ372067
VERSION BJ372067.1 GI:19281450
KEYWORDS EST.
SOURCE Dictyostelium discoideum.
ORGANISM Dictyostelium discoideum
REFERENCE 1 (bases 1 to 651)
AUTHORS Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-I,T.
TITLE Full length cDNA of Dictyostelium discoideum at the culmination
stage
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-i
```

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National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.

FEATURES
Location/Qualifiers
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/organism="Dictyostelium discoideum"
/strain="AX4"
/db_xref="taxon:44689"
/clone="ddc1k04"
/clone_lib="Dictyostelium discoideum cdna library, CF"
/sex="mat A"
/dev_stage="Culmination stage"

BASE COUNT 191 a 124 c 113 g 223 t
ORIGIN

Query Match 3.0%; Score 57.2; DB 13; Length 651;
Best Local Similarity 45.1%; Pred. No. 3.9e-05;
Matches 264; Conservative 0; Mismatches 313; Indels 9; Gaps 1;

Qy 1324 AAAAAGTGGTGGTTTCGTTACCGACAAATGTATCCCACTTGACATTTTCACCACT 1383
Db 634 AAATACATTTGTTGCAATTCACCAACATTTGGCTGGCGGTATTCATTTATCACCATCT 575

Qy 1384 CTTCCCGCGAGAACGATTCGGCGGAAAAATCTATCCTCGCTACTATAGCAAGATA 1443
Db 574 ATGCCACCAAGACGTGATGAATCCTCAAGAAATGCCAATGGTTCGTCATTAACACC 515

Qy 1444 GTCTTCGTATGGGACAAACCGTGGTGGCGGACAAAGCTTCTCGGCGTCTCCCAATCG 1503
Db 514 ATCACCATCTATGATGAACCATTTCTGGAGAAAGAGGTTATTTCAGCTGAAGCCATCTCT 455

Qy 1504 AGCTGTGACCCCATCTCATTTGCCAGAGATACCAAGTCGATCGCAATGGTCC 1563
Db 454 GATAAAGGTCCAAATCTTATCTGTATGATGACTCTTCACATGACGATAGAAACAGCT 395

Qy 1564 ATTACCTGTTTCATGTCGGAGACCGGAGGAGTGGTCCCAACAGTCCCAAGCAGGTA 1623
Db 394 ATCGTTGTTTCATGCTGCTTTCAGCCGCTTAAGATTTGGCTGAAATATCACCAGAGAA 335

Qy 1624 CGACAAAAGTCTGTCTGGGCAACTCCGCGCAGCCTACGAGAACGCCGGGCCCCAAGTC 1683
Db 334 AGAAAGAGAGCGCTTAGACTGTTATGCTCGTTGGT-----GGGGTCCAAAAGCA 284

Qy 1684 CCAGAGCGGCGCAAGCTGCTCAATCGATGGTTCGAGCAGCAGTATTTCCAAAGGAGCT 1743
Db 283 TTATCTCCAAGAATCTTTTAGAGAAAAGTTGGAAGAAAGAAATATTCACGTGGTGT 224

Qy 1744 CCGAGCGCGTCTATGGGCTGAACGATCTCATCACACTGGTTCGGCGCTCAGAACCGCG 1803
Db 223 TATTAGTTTACACTAGTCCAGGTACTCTTACCATGTGGTGAACATTTACGTGCTCCA 164

Qy 1804 TTCAAGTGTGTTCAATTTGGTGGAAACGAGACGTCTTTAGTTTGGAAAGGTATATGGAA 1863
Db 163 GTTGGTAGAATTCATTTGGGCTGGTACAGAACTGCTTCAGTTTGGATTGGTTATATGGAA 104

Qy 1864 GGGGCCATACGATCGGTCACAGAGTCTGCAGAAAGTTGTGGCTA 1909
Db 103 GGTGCCCTTAGAATCAGGTTTATAGAGTTTCAAAAAGAAATTAAGATA 58

RESULT 12
BJ430839/c 658 bp mRNA linear EST 13-MAR-2002
LOCUS BJ430839 Dictyostelium discoideum cdna library, VF Dictyostelium
DEFINITION dictyostelium cdna clone ddc9b03 3', mRNA sequence.
ACCESSION BJ430839
VERSION BJ430839.1 GI:19405561
KEYWORDS EST.
SOURCE Dictyostelium discoideum.
ORGANISM Dictyostelium discoideum
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[illegible]

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| DEFINITION | BJ374842 Dictyostellium discoideum cDNA library, CF Dictyostellium discoideum cDNA clone ddc16b17 3', mRNA sequence. | | | | | | | | | |
| ACCESSION | BJ374842 | | | | | | | | | |
| VERSION | BJ374842.1 GI:19284225 | | | | | | | | | |
| KEYWORDS | EST. | | | | | | | | | |
| SOURCE | Dictyostellium discoideum. | | | | | | | | | |
| ORGANISM | Dictyostellium discoideum | | | | | | | | | |
| REFERENCE | Eukaryota; Mycetozoa; Dictyostellida; Dictyostellium. | | | | | | | | | |
| AUTHORS | Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T. | | | | | | | | | |
| TITLE | Full length cDNA of Dictyostellium discoideum at the culmination stage | | | | | | | | | |
| JOURNAL | Unpublished (2002) | | | | | | | | | |
| COMMENT | Contact: Tadasu Shin-i Center for Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856 Fax: 81-559-81-6855 Email: tshini@genes.nig.ac.jp. | | | | | | | | | |
| FEATURES | Location/Qualifiers | | | | | | | | | |
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| | /organism="Dictyostellium discoideum" | | | | | | | | | |
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| | /clone_lib="Dictyostellium discoideum cDNA library, CF" | | | | | | | | | |
| | /sex="mat A" | | | | | | | | | |
| | /dev_stage="Culmination stage" | | | | | | | | | |
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| ORIGIN | | | | | | | | | | |
| Query Match | 3.0%; Score 57.2; DB 13; Length 686; | | | | | | | | | |
| Best Local Similarity | 44.1%; Pred. No. 4.le-05; | | | | | | | | | |
| Matches | 294; | Conservative | 0; | Mismatches | 363; | Indels | 9; | Gaps | | |
| Qy | 1244 | TCACACCCCCGTCGCTGGAAATTGAGCAGTCGGCGCTGTATAGTACGATCGGCCT | 1303 | | | | | | | |
| Db | 672 | TAAATGACCAAGTCGGTTCATATTCAAGATGCCAATCATGTACCAATTAACACTGATA | 613 | | | | | | | |
| Qy | 1304 | CGGCGCGCGTTCGGAAGCAAAAAGTGGTGGTTTCGTACCGACACACATGTATCCCA | 1363 | | | | | | | |
| Db | 612 | ACGTTCACTTATCGTTCAAATACATATGTTGTTCGAATTCACCAACATTTGGCTGCC | 553 | | | | | | | |
| Qy | 1364 | CCTTGACATTTTCCACACCTCTTCGCCGCGAAGCAAGCATTTGGCGAAAAATCTATCC | 1423 | | | | | | | |
| Db | 552 | GTATTCTATTATCAACCATCTATGCCACCAAGACGTGATGAATCACTCAAGAATGCCAA | 493 | | | | | | | |
| Qy | 1424 | TCGGCTACTATACAGATAGTCTTCGTATGGGACACCCGTGGTGGCGGACACAGGCT | 1483 | | | | | | | |
| Db | 492 | TGGTTCGCGTCATTAACACCATCACCATCTATGATGAACCATTTGGAGAAAAGAAGTT | 433 | | | | | | | |
| Qy | 1484 | TCTCGGGCGTCTCCCAATCGAGCTGTGACCCCATCTCAATTTGCCAGAGATACCAAGTCG | 1543 | | | | | | | |
| Db | 432 | ATTCAAGTGAAGCCATCTCTGATAAGGTCCCAATCTTTATCTGTAATGATGACTCTCAC | 373 | | | | | | | |
| Qy | 1544 | AAGTCGATCGGCAATGGTCCATTAACCTGTTTCATGGTCGGAGACCCGGGACGGAAGTGT | 1603 | | | | | | | |
| Db | 372 | ATGACGATAGAAAACAGCATATCGTTGGTTTTCATTTGCTTCAGCGCTAAAGATTGGG | 313 | | | | | | | |
| Qy | 1604 | CCCAACAGTCCAAGCAGGTACGACAAAAGTCTGTCTGGAGCCCACTCGGCGCAGCCTACG | 1663 | | | | | | | |
| Db | 312 | CTGAAAATCACCAGAAAGAAAGACAGCGCTTTAGACTGTTATGCTGTTGGTGGG | 253 | | | | | | | |
| Qy | 1664 | AGAACGCGGGGCCCCAAGTCCACAGACCGGCCAACGTCCTCGAAATCGATGGTGCNAAGC | 1723 | | | | | | | |
| Db | 252 | -----GTCCAAAGCATTAATCCCAAGAAATCTTTTAGAGAAAAGTTGGAAAAGAG | 202 | | | | | | | |
| Qy | 1724 | ACGAGTATTTCAAGGAGCTCCGACCGCGTCTATGGCGCTGAACGATCTCATCACACTGG | 1783 | | | | | | | |
| Db | 201 | AGAATATTCAAGTGGTGTATTATAGTTACACTAGTCCAGGTACTCTTACCAATGTG | 142 | | | | | | | |
| Qy | 1784 | GTTCCGCGCTCAGAACCGCGTTTCAAGTGTGTTCATTTTCGTTGAACGAGACGCTTTTAG | 1843 | | | | | | | |


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Db 141 GTGAACATTACGTGCTCAGTGTGTAGAAATTTCATTTGGCTGGGTACAGAAACTGCTTCAG 82
Qy 1844 TTTGGAAAGGTTATATGGAAGGGCCATACGATCGGTCAACAGAGGTGCTGCAGAAAGTTG 1903
Db 81 TTTGGATTGTTATATGGAAGGTGCTTGAATCAGAGTTTATAGAGTTTCAAAAGAAATTA 22
Qy 1904 TGGCTA 1909
Db 21 AAGATA 16

RESULT 14
BJ429162/c 687 bp mRNA linear EST 13-MAR-2002
LOCUS BJ429162 Dictyostelium discoideum cDNA library, VF Dictyostelium
DEFINITION BJ429162 Dictyostelium discoideum cDNA clone ddv2f15 3', mRNA sequence.
ACCESSION BJ429162.1 GI:19403884
VERSION BJ429162
KEYWORDS EST.
SOURCE Dictyostelium discoideum.
ORGANISM Dictyostelium discoideum.
REFERENCE 1 (bases 1 to 687)
AUTHORS Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
TITLES Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
Full length cDNA of Dictyostelium discoideum at the vegetative
stage
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
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BASE COUNT 202 a 135 c 129 g 221 t
ORIGIN
Query Match 3.0%; Score 57.2; DB 13; Length 687;
Best Local Similarity 44.1%; Pred. No. 4.1e-05;
Matches 294; Conservative 0; Mismatches 363; Indels 9; Gaps 1;

Qy 1244 TCAACACCCCGTGGTGGAAATTGAGCAGTCGGCGTCCGGCTGTATAGTACGATCGGCCT 1303
Db 672 TAAATGCCACGAGTCGTTCCATTATTCAAGATGCCAATCAATGTACCATTAATAACTGATA 613
Qy 1304 CGGGCGGCGTGTCCGAAGCAAAAGGTGGTGTTCGTTACCGACACACATTGTATCCCA 1363
Db 612 ACGGTTCAACTTATCGTTCAAATACATATGTTGCCATTCCACACATTGGCTGCC 553
Qy 1364 CTTGACATTTTACCAACACCTCTCCCGCGGAGAACGATTCGGGGAATAATCTATCC 1423
Db 552 GTATTTCATTATTCACCATCTATGCCAACAGAGCTGTATGAACCTCACTCAAGAATGCCAA 493
Qy 1424 TCGGCTACTATAGCAAGATAGTCTTCGTATGGACAACCGTGGTGGCGGCAACAGGCT 1483
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Qy 1544 AAGTCGATCGCAATGGTTCATTACCTGTTTCATGTCGAGACCGGGACGGAAGTGGT 1603

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Db 372 ATGACGATAAGAAAACAGCTATCGTTGGTTTCATTGCTGCTTACGCCCTAAAGATTGGG 313
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Qy 1844 TTTGGAAGGTTATATGGAAGGGCCATACGATCGGTCAACAGAGGTGCTGCAGAAAGTTG 1903
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Qy 1904 TGGCTA 1909
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RESULT 15
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LOCUS BJ375168 Dictyostelium discoideum cDNA library, CF Dictyostelium
DEFINITION BJ375168 Dictyostelium discoideum cDNA clone ddcl7n18 3', mRNA sequence.
ACCESSION BJ375168
VERSION BJ375168
KEYWORDS EST.
SOURCE Dictyostelium discoideum.
ORGANISM Dictyostelium discoideum.
REFERENCE 1 (bases 1 to 694)
AUTHORS Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
TITLES Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
Full length cDNA of Dictyostelium discoideum at the culmination
stage
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
FEATURES
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/db_xref="taxon:44689"
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Query Match 3.0%; Score 57.2; DB 13; Length 694;
Best Local Similarity 45.1%; Pred. No. 4.1e-05;
Matches 264; Conservative 0; Mismatches 313; Indels 9; Gaps 1;

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Db 561 ATGCCACCAAGACGTGATGAATCACTCAAAAGATGCCAATGGTTCGTCATTAATACC 502

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Db 501 ATCACCATCTATGATGNACCATTCCTGGAGAAAAGAGTTATTGAGCTGAAGCCATCTCT 442
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QY 1504 AGCTGTGACCCCATCTCATTTGGCCAGAGATACCAAGTCGAAGTCGATCGGCAATGGTCC 1563
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Db 441 GATAAAGTCCCAATCTTTATCTGCTATGATGACTCTTCACATGACGATAAGAAAACAGCT 382
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QY 1564 ATTACCTGTTTCATGTGTCGGAGACCGGACGGAAGTGTGCCACACAGTCCCAAGCAGGTA 1623
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Db 381 ATCGTTGGTTTCATTTGCTGCTTCAGCCGCTAAAGATTGGGCTGAAAATCACCAGAAAGAA 322
   || || || || || || || || || || || || || || || || || || ||
QY 1624 CGACAAAAGTCTGTCTGGGACCAACTCCCGCAGCCTACGAGACGCCGGGGCCCCAAGTC 1683
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Db 321 AGAAGAGAGAGCCGCTTAGACTGTTATGCTCGTTGGT-----GGGGTCCAAAAGCA 271
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QY 1684 CCAGAGCCGGCCACGCTGCTCGAAATCGAGTGGTCGAAGCAGCAGTATTTCCAAAGGAGCT 1743
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QY 1744 CCGAGCCCGCTATGGGCTGACGATCTCATCACACTGGGTCGGCGCTCAGAACCCG 1803
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Search completed: November 12, 2002, 05:30:41
Job time : 2825 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 12, 2002, 03:18:45 ; Search time 77 Seconds
(without alignments)
7682.850 Million cell updates/sec

Title: US-09-771-045A-35
Perfect score: 1929
Sequence: 1 atggcaactgacccagagcta.....gcctgggtgccagagcatag 1929

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|------------------|
| 1 | 1929 | 100.0 | 1929 | 4 | US-09-352-159-35 |
| 2 | 1925.8 | 99.8 | 1929 | 4 | US-09-352-159-37 |
| 3 | 1851.4 | 96.0 | 1930 | 4 | US-09-352-159-39 |
| 4 | 1792.2 | 92.9 | 1928 | 4 | US-09-352-159-43 |
| 5 | 1789 | 92.7 | 1928 | 4 | US-09-352-159-45 |
| 6 | 1787.4 | 92.7 | 1928 | 4 | US-09-352-159-41 |
| 7 | 1602.6 | 83.1 | 1803 | 4 | US-09-352-159-22 |
| 8 | 1602.6 | 83.1 | 1803 | 4 | US-09-352-168-22 |
| 9 | 1596.2 | 82.7 | 2490 | 4 | US-09-352-159-32 |
| 10 | 1596.2 | 82.7 | 2490 | 4 | US-09-352-168-32 |
| 11 | 1319 | 68.4 | 1442 | 4 | US-09-352-159-7 |
| 12 | 1319 | 68.4 | 1442 | 4 | US-09-352-168-7 |
| 13 | 1212.2 | 62.8 | 2976 | 4 | US-09-352-159-26 |
| 14 | 1212.2 | 62.8 | 2976 | 4 | US-09-352-168-26 |
| 15 | 1212.2 | 62.8 | 3003 | 4 | US-09-352-159-24 |
| 16 | 1212.2 | 62.8 | 3003 | 4 | US-09-352-168-24 |
| 17 | 1212.2 | 62.8 | 3591 | 4 | US-09-352-159-30 |
| 18 | 1212.2 | 62.8 | 3591 | 4 | US-09-352-168-30 |
| 19 | 1212.2 | 62.8 | 3618 | 4 | US-09-352-159-28 |
| 20 | 1212.2 | 62.8 | 3618 | 4 | US-09-352-168-28 |
| 21 | 1212 | 62.8 | 1392 | 4 | US-09-352-159-10 |
| 22 | 1212 | 62.8 | 1392 | 4 | US-09-352-168-10 |
| 23 | 1212 | 62.8 | 1464 | 4 | US-09-352-159-20 |
| 24 | 1212 | 62.8 | 1464 | 4 | US-09-352-168-20 |
| 25 | 1212 | 62.8 | 1673 | 4 | US-09-352-159-16 |
| 26 | 1212 | 62.8 | 1673 | 4 | US-09-352-168-16 |
| 27 | 1212 | 62.8 | 2079 | 4 | US-09-352-159-18 |

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| 28 | 1212 | 62.8 | 2079 | 4 | US-09-352-168-18 | Sequence 18, Appl |
| 29 | 1211 | 62.8 | 1389 | 4 | US-09-352-159-5 | Sequence 5, Appli |
| 30 | 1211 | 62.8 | 1389 | 4 | US-09-352-168-5 | Sequence 5, Appli |
| c 31 | 361.4 | 18.7 | 372 | 4 | US-09-352-159-1 | Sequence 1, Appli |
| c 32 | 361.4 | 18.7 | 372 | 4 | US-09-352-168-1 | Sequence 1, Appli |
| c 33 | 174 | 9.0 | 182 | 4 | US-09-352-159-2 | Sequence 2, Appli |
| c 34 | 174 | 9.0 | 182 | 4 | US-09-352-168-2 | Sequence 2, Appli |
| 35 | 36.6 | 1.9 | 1575 | 4 | US-09-230-388-2 | Sequence 1, Appli |
| 36 | 35.8 | 1.9 | 50937 | 4 | US-09-428-517-1 | Sequence 31, Appl |
| c 37 | 34.8 | 1.8 | 1964 | 1 | US-08-132-168A-31 | Sequence 374, App |
| c 38 | 34.4 | 1.8 | 405 | 4 | US-09-199-637A-374 | Sequence 372, App |
| c 39 | 34.4 | 1.8 | 603 | 4 | US-09-199-637A-372 | Sequence 366, App |
| c 40 | 34.4 | 1.8 | 1137 | 4 | US-09-199-637A-366 | Sequence 1, Appli |
| c 41 | 34.4 | 1.8 | 42235 | 4 | US-09-199-637A-1 | Sequence 15, Appl |
| c 42 | 34.2 | 1.8 | 7295 | 2 | US-08-487-826B-15 | Sequence 15, Appl |
| c 43 | 34 | 1.8 | 2068 | 4 | US-09-318-448-15 | Sequence 15, Appl |
| c 44 | 33.6 | 1.7 | 2346 | 4 | US-09-149-476-193 | Sequence 193, App |
| c 45 | 33.2 | 1.7 | 2743 | 4 | US-09-060-482-3 | Sequence 3, Appl |

ALIGNMENTS

RESULT 1
US-09-352-159-35
; Sequence 35, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
; FILE REFERENCE: 1134
; CURRENT APPLICATION NUMBER: US/09/352,159A
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: 60/092,936
; EARLIER FILING DATE: 1998-07-25
; EARLIER APPLICATION NUMBER: 60/135,391
; EARLIER FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 35
; LENGTH: 1929
; TYPE: DNA
; ORGANISM: Exophiala spinifera
; FEATURE:
; NAME/KEY: Intron
; LOCATION: (739)...(811)
; NAME/KEY: Intron
; LOCATION: (1134)...(1186)
US-09-352-159-35

Query Match 100.0%; Score 1929; DB 4; Length 1929;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1929; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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| Db | 1 | ATGGCACTTGCACCGAGCTACATCAATCCCAAGAGTTCCTCCCGAGGATATCC | 60 |
| QY | 61 | CACATCGGCTAGCGCCAAACGAGGATGTGACATAGCTGGACAGATTGGACAA | 120 |
| Db | 61 | CACATCGGCTAGCGCCAAACGAGGATGTGACATAGCTGGACAGATTGGACAA | 120 |
| QY | 121 | GAGCCTTGGCGCTGACAGACCCAGCTAGGAGAAACAGTTCGCCCAAGCATTCGCAAT | 180 |
| Db | 121 | GAGCCTTGGCGCTGACAGACCCAGCTAGGAGAAACAGTTCGCCCAAGCATTCGCAAT | 180 |
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| Db | 181 | CTGCGAGCTTGCCTTGTGCTGAGTTGGAGCCTCTTCAACAGACGTCAACAGCTCAATTAC | 240 |

QY 241 TACATCGTCGACTACGCCCGAGCAAACTCACCGCAATTCGAGATGGGTGAAGTCTACC 300
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Db 1201 TGCCATGCCATGTCAAAGGAATTTGTTCCAGGCTCAGTCACCTCAACACCCCGCTGCT 1260
QY 1261 GGAATTGAGCAGTCGGGCTCCGGCTGTATATAGTACGATCGGCGCGGCTTTCCGA 1320
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Db 1261 GGAATTGAGCAGTCGGGCTCCGGCTGTATATAGTACGATCGGCTCGGCGCGGCTTTCCGA 1320
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QY 1741 GCTCGAGCGCGCTCTATGGGCTGAACGATCTCATCAGCTGGGTTTCGCGCTCAGAACG 1800
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Db 1741 GCTCGAGCGCGCTCTATGGGCTGAACGATCTCATCAGCTGGGTTTCGCGCTCAGAACG 1800
QY 1801 CCGTTCAAGTGTGTTCATTTTCGTTGGAAACGAGACGCTTTTAGTTTGGAAAGGTTATATG 1860
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Db 1801 CCGTTCAAGTGTGTTCATTTTCGTTGGAAACGAGACGCTTTTAGTTTGGAAAGGTTATATG 1860
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QY 1921 GCAGCATAG 1929
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RESULT 2

US-09-352-159-37
; Sequence 37, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Madrox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
; FILE REFERENCE: 1134
; CURRENT APPLICATION NUMBER: US/09/352,159A
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: 60/092,936
; EARLIER FILING DATE: 1998-07-25
; EARLIER APPLICATION NUMBER: 60/135,391
; EARLIER FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 37
; LENGTH: 1929
; TYPE: DNA
; ORGANISM: Exophiala spinifera
; FEATURE:
; NAME/KEY: intron
; LOCATION: (739)...(811)
; NAME/KEY: intron
; LOCATION: (1134)...(1186)
US-09-352-159-37

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| Query Match | | | | | | | | | |
| Best Local Similarity 99.9%; Score 1925.8; DB 4; Length 1929; | | | | | | | | | |
| Matches 1927; Conservative 0; Mismatches 2; Indels 0; Gaps 0; | | | | | | | | | |
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| Db | 61 | CACATCGGGGTAGGGCCCAACCAAGCGAGGTATGTGACAATAGCTGGACAGATTGGACAA | 120 | | | | | | |
| QY | 121 | GACGCTTTGGGCGTGACAGACCCAGCCCTACGAGAAACAGGTTGCCCAAGCAATTGCGCCAAT | 180 | | | | | | |
| Db | 121 | GACGCTTTGGGCGTGACAGACCCAGCCCTACGAGAAACAGGTTGCCCAAGCAATTGCGCCAAT | 180 | | | | | | |
| QY | 181 | CTGGCAGCTTGCCTTGTCTGCACTTGGAGCTTTCCTTGCAGCTGTGCGAGTACCAAGCTCAATTAC | 240 | | | | | | |
| Db | 181 | CTGGCAGCTTGCCTTGTCTGCACTTGGAGCTTTCCTTGCAGCTGTGCGAGTACCAAGCTCAATTAC | 240 | | | | | | |
| QY | 241 | TACATCGTGCAGTACGCCCGGAGCAAACTCACCGCAATTGGAGATGGGCTGAAGTCTACC | 300 | | | | | | |
| Db | 241 | TACATCGTGCAGTACGCCCGGAGCAAACTCACCGCAATTGGAGATGGGCTGAAGTCTACC | 300 | | | | | | |
| QY | 301 | TTTGCCCTTGACAGGCTCCCTCCTTGCAGCTGTGCGAGTACCGGCTTGGCTTCACT | 360 | | | | | | |
| Db | 301 | TTTGCCCTTGACAGGCTCCCTCCTTGCAGCTGTGCGAGTACCGGCTTGGCTTCACT | 360 | | | | | | |
| QY | 361 | GAATACCTTTTTCAGTGTGATCCACGGCGGTGGTGCCAGACACTCACGCCCGAGCAAC | 420 | | | | | | |
| Db | 361 | GAATACCTTTTTCAGTGTGATCCACGGCGGTGGTGCCAGACACTCACGCCCGAGCAAC | 420 | | | | | | |
| QY | 421 | GTTCGGGAGCTGTAGTGTGGGCGCTGGCTTTCAGCGTGTGGAGCGGCGACGCAAAAGTC | 480 | | | | | | |
| Db | 421 | GTTCGGGAGCTGTAGTGTGGGCGCTGGCTTTCAGCGTGTGGAGCGGCGACGCAAAAGTC | 480 | | | | | | |
| QY | 481 | CAGGCGCGCGGTCTGTCTGCGCTCTTTCAGGCGCATGGATCGGTAGGGGGAAGACT | 540 | | | | | | |
| Db | 481 | CAGGCGCGCGGTCTGTCTGCGCTCTTTCAGGCGCATGGATCGGTAGGGGGAAGACT | 540 | | | | | | |
| QY | 541 | CTGAGGTACAACTCGGTCGCGGAGGAGCTATCAACGACCTCGGCGCTGCGTGGATC | 600 | | | | | | |
| Db | -541 | CTGAGGTACAACTCGGTCGCGGAGGAGCTATCAACGACCTCGGCGCTGCGTGGATC | 600 | | | | | | |
| QY | 601 | AATGACAGCAACAAAGCGAAGTATCCAGATTGTTTGAAGATTTCATTTGGAGGGCGAG | 660 | | | | | | |
| Db | 601 | AATGACAGCAACAAAGCGAAGTATCCAGATTGTTTGAAGATTTCATTTGGAGGGCGAG | 660 | | | | | | |
| QY | 661 | CTCCAGAGACGACCGGAAATTCATTCATCAAGCACAGCGGTACAAACCACTACAGCT | 720 | | | | | | |
| Db | 661 | CTCCAGAGACGACCGGAAATTCATTCATCAAGCACAGCGGTACAAACCACTACAGCT | 720 | | | | | | |
| QY | 721 | CCTTATGTTAGTCCCGGTAGACACATCCCACTTTTGTATGAGACCTCTGCGAGTGT | 780 | | | | | | |
| Db | 721 | CCTTATGTTAGTCCCGGTAGACACATCCCACTTTTGTATGAGACCTCTGCGAGTGT | 780 | | | | | | |
| QY | 781 | AGAATACAGTCACTGACTCCACTTCGTCAGCTGAGCGGAGGTTGCAAGTGCACATTGC | 840 | | | | | | |
| Db | 781 | AGAATACAGTCACTGACTCCACTTCGTCAGCTGAGCGGAGGTTGCAAGTGCACATTGC | 840 | | | | | | |
| QY | 841 | GGAATCTCTCCCGTATGGTCTCAGCTGATCGAAGAGTATAGCCCTTGAAGACCCCAAGGC | 900 | | | | | | |
| Db | 841 | GGAATCTCTCCCGTATGGTCTCAGCTGATCGAAGAGTATAGCCCTTGAAGACCCCAAGGC | 900 | | | | | | |
| QY | 901 | GAGCCCTCAGGCGAAGCGGCTGCAGATGTGAGCTTCCGCGCACTACTGTGAGAAGGACCT | 960 | | | | | | |
| Db | 901 | GAGCCCTCAGGCGAAGCGGCTGCAGATGTGAGCTTCCGCGCACTACTGTGAGAAGGACCT | 960 | | | | | | |
| QY | 961 | AAACTTGCTGCTGTCTCAGCGTGGCAAAACAGATACACGCGCTCTGCTCGGTGTGGA | 1020 | | | | | | |
| Db | 961 | AAACTTGCTGCTGTCTCAGCGTGGCAAAACAGATACACGCGCTCTGCTCGGTGTGGA | 1020 | | | | | | |

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| QY | 1021 | AGCCACGAGATCAGCATGCTTTTTCTCACCGACTACATCAAGAGTCCCAACCGGTCTCAG | 1080 |
| Db | 1021 | AGCCACGAGATCAGCATGCTTTTTCTCACCGACTACATCAAGAGTCCCAACCGGTCTCAG | 1080 |
| QY | 1081 | TAATATTGTCGCGACAAGAAAGACGGCGGCGAGTATATCGATGCAAAACAGGTGCGTG | 1140 |
| Db | 1081 | TAATATTGTCGCGACAAGAAAGACGGCGGCGAGTATATCGATGCAAAACAGGTGCGTG | 1140 |
| QY | 1141 | CGGTGCTCTCTCAGGTAGGGACTCGTTTCTTAGTGTGCTATTCCAGGTATGCAATCGATT | 1200 |
| Db | 1141 | CGGTGCTCTCTCAGGTAGGGACTCGTTTCTTAGTGTGCTATTCCAGGTATGCAATCGATT | 1200 |
| QY | 1201 | TGCCATGCCATGTCAAAGAACTTGTTCAGGCTCAGTGCACCTCAACACCCCGCTCGCT | 1260 |
| Db | 1201 | TGCCATGCCATGTCAAAGAACTTGTTCAGGCTCAGTGCACCTCAACACCCCGCTCGCT | 1260 |
| QY | 1261 | GGATTGAGCAGTCGGGCTCGGCTGTATAGTACGATCGGCTCGGCGCGCTGTTCCGA | 1320 |
| Db | 1261 | GGATTGAGCAGTCGGGCTCGGCTGTATAGTACGATCGGCTCGGCGCGCTGTTCCGA | 1320 |
| QY | 1321 | AGCAAAAAGTGTGTTCGTTTACCGACAACATTTGATCCCACTTGACATTTTCACCA | 1380 |
| Db | 1321 | AGCAAAAAGTGTGTTCGTTTACCGACAACATTTGATCCCACTTGACATTTTCACCA | 1380 |
| QY | 1381 | CCTTTCCTCCCGAGAAAGCATTTGGCGGAAAAATCTATCCTCGGCTACTATAGCAAG | 1440 |
| Db | 1381 | CCTTTCCTCCCGAGAAAGCATTTGGCGGAAAAATCTATCCTCGGCTACTATAGCAAG | 1440 |
| QY | 1441 | ATAGTCTTCGTATGGGACAACCGTGTGTGGCGGACAAGGCTTCTCGGCGCTCTCCAA | 1500 |
| Db | 1441 | ATAGTCTTCGTATGGGACAACCGTGTGTGGCGGACAAGGCTTCTCGGCGCTCTCCAA | 1500 |
| QY | 1501 | TCGAGCTGTGACCCCATCTCATTTGCCAGAGATACCAGCATCGAAGTCGCAATGG | 1560 |
| Db | 1501 | TCGAGCTGTGACCCCATCTCATTTGCCAGAGATACCAGCATCGAAGTCGCAATGG | 1560 |
| QY | 1561 | TCCATTACCTGTTTCATGTGCGGAGACCCGGGACGGAAAGTGGTCCCAACAGTCCAAAGCAG | 1620 |
| Db | 1561 | TCCATTACCTGTTTCATGTGCGGAGACCCGGGACGGAAAGTGGTCCCAACAGTCCAAAGCAG | 1620 |
| QY | 1621 | GTACGACAAAAGTCTGTCTGGGACCACTCCGGCGAGCTTACGAGAACGCCGGGCCAA | 1680 |
| Db | 1621 | GTACGACAAAAGTCTGTCTGGGACCACTCCGGCGAGCTTACGAGAACGCCGGGCCAA | 1680 |
| QY | 1681 | GTCCACAGCGCGGCAACAGTCTCGAAATCGAGTGTGCGAAGCAGAGTATTTCCAAGGA | 1740 |
| Db | 1681 | GTCCACAGCGCGGCAACAGTCTCGAAATCGAGTGTGCGAAGCAGAGTATTTCCAAGGA | 1740 |
| QY | 1741 | GCTCCGAGCGCGCTCTATGGGCTGAACGATCTCATCACTGGGTTCCGGCTCAGAAGC | 1800 |
| Db | 1741 | GCTCCGAGCGCGCTCTATGGGCTGAACGATCTCATCACTGGGTTCCGGCTCAGAAGC | 1800 |
| QY | 1801 | CGGTTCAAGTGTGTTTCATTTGCGTTGGAACGAGAGCTCTTTTACGTTGGAAGGTTATG | 1860 |
| Db | 1801 | CGGTTCAAGTGTGTTTCATTTGCGTTGGAACGAGAGCTCTTTTACGTTGGAAGGTTATG | 1860 |
| QY | 1861 | GAAGGGCCATACGATCGGCTCAACGAGGTCGCAAGTTCGTGCTAGCTGCTGCTGCA | 1920 |
| Db | 1861 | GAAGGGCCATACGATCGGCTCAACGAGGTCGCAAGTTCGTGCTAGCTGCTGCTGCA | 1920 |
| QY | 1921 | GCAGCATAG 1929 | |
| Db | 1921 | GCAGCATAG 1929 | |

RESULT 3
US-09-352-159-39
; Sequence 39, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
; APPLICANT: DuVick, Jonathan P.
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.

```
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
; FILE REFERENCE: 1134
; CURRENT APPLICATION NUMBER: US/09/352,159A
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: 60/092,936
; EARLIER FILING DATE: 1998-07-25
; EARLIER APPLICATION NUMBER: 60/135,391
; EARLIER FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 39
; LENGTH: 1930
; TYPE: DNA
; ORGANISM: Exophiala spinifera
; FEATURE:
; NAME/KEY: Intron
; LOCATION: (739)...(811)
; NAME/KEY: Intron
; LOCATION: (1134)...(1187)
; NAME/KEY: misc.feature
; LOCATION: (648)...(648)
; OTHER INFORMATION: n = A,T,C or G
US-09-352-159-39
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Query Match          96.0%; Score 1851.4; DB 4; Length 1930;
Best Local Similarity 97.8%; Pred. No. 0;
Matches 1887; Conservative 0; Mismatches 42; Indels 1; Gaps 1;

QY 1 ATGGCACTTGCACCGAGCTACATCAATCCCCAAACGTCGCGCTCCCGAGCAGGATATTC 60
Db 1 ATGGCACTTGCACCGAGCTACATCAATCCCCAAACGTCGCGCTCCCGAGCAGGATATTC 60

QY 61 CACATCGGCGTAGGCCCAACCAAGCGAGGTATGTGACATAGCTGGACAGATTGGACAA 120
Db 61 CACGTGCGGCTAGGCCCAACCAAGCGAGGTATGTGACATAGCTGGACAGATTGGACAA 120

QY 121 GACGCTTTGGGGGTGACAGACCCAGCCTACGAGAAACAGGTTGCCCAAGCATTCGCCAAT 180
Db 121 GACGCTTTGGGGGTGACAGACCCAGCCTACGAGAAACAGGTTGCCCAAGCATTCGCCAAT 180

QY 181 CTGCGAGCTTGGCTTGCAGTTGAGGCTCTTCAACAGAGGTGACCAAGCTCAATATAC 240
Db 181 CTGCGAGCTTGGCTTGCAGTTGAGGCTCTTCAACAGAGGTGACCAAGCTCAATATAC 240

QY 241 TACATCGTCGACTACGCCCGGAGCAACTCACCGCAATTGGAGATGGCTGAAGTCTACC 300
Db 241 TACATCGTCGACTACGCCCGGAGCAACTCACCGCAATTGGAGATGGCTGAAGTCTACC 300

QY 301 TTGCGCCTTGACAGGCTCCCTCTTGCAGGCTGGTGCAGTACCGGCGCTTGGCTTCACT 360
Db 301 TTGCGCCTTGACAGGCTCCCTCTTGCAGGCTGGTGCAGTACCGGCGCTTGGCTTCACT 360

QY 361 GAATACCTTTGAGGTGATGCCAGCGGCTGGTGCAGGACACTCGACCCGAGACAAAC 420
Db 361 GAATACCTTTGAGGTGATGCCAGCGGCTGGTGCAGGACACTCGACCCGAGACAAAC 420

QY 421 GTTGGCGAGTGTAGTGTGGGCGCTGGCTTGAAGGTTGGAGACGCGCAAGATC 480
Db 421 GTTGGCGAGTGTAGTGTGGGCGCTGGCTTGAAGGTTGGAGACGCGCAAGATC 480

QY 481 CAGGCGCGCGGCTGTCTCTCGCTTCTTGAAGCGGATGGATCGTGTAGGGGGAAGACT 540
Db 481 CAGGCGCGCGGCTGTCTCTCGCTTCTTGAAGCGGATGGATCGTGTAGGGGGAAGACT 540

QY 541 CTGAGCGTACATTCGGGTCGCCGAGGAGGACTATCAACGACCTCGGCGCTGGGTGATC 600
Db 541 CTGAGCGTACATTCGGGTCGCCGAGGAGGACTATCAACGACCTCGGCGCTGGGTGATC 600

QY 601 AATGACAGCAACCAAGCGAAGTATCCAGATTGTTGAAAGATTTCATTTGAGGGCCAG 660
Db 601 AATGACAGCAACCAAGCGAAGTATCCAGATTGTTGAAAGATTTCATNTGAGGGCCAG 660
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QY 661 CTCAGAGGACGACCGGAAATTCATCCATCAAGCACAAAGACGGTACAAACCACTACAGCT 720
Db 661 CTCAGAGGACGACTGGAATTCATCCATCAAGCACAAAGACGGTACAAACCACTACAGCT 720

QY 721 CCTTATGGTGACTCCCGGGTAAGCACAAATCCCACCTTTGTGATGAGACCTCTGTGCGAGTGT 780
Db 721 CCTTATGGTGACTCCCTTGGTAAGCACAAATCCCACCTTTGTGATGAGACCTCTGTGCGAGTGT 780

QY 781 AGAATACAGTCACTGACTCCACTTCGTCAGCTGAGCGGAGGAGTTGCAAGTGCACCTTGC 840
Db 781 AGAATACAGTCACTGATTCACCTTCGTCAGCTGAGCGGAGGAGTTGCAAGTGCACCTTGC 840

QY 841 GGAACCTCTCCCGTATGTGCTCAGCTGATCGAAGAGTATAGCTTTGAAGACCCCAAGGC 900
Db 841 GGAACCTCTCCCGTATGTGCTCAGCTGATCGAAGAGTATAGCTTTCAAGACCTCAAGGC 900

QY 901 GAGCCCTCAGCGGAAGCGGCTCGACAGTGTGAGCTTCGGCGCACTACTGTGAGAAGACCT 960
Db 901 GAGCCCTCAGCGGAAGCGGCTCGACAGTGTGAGCTTCGGCGCACTACTGTGAGAAGAACT 960

QY 961 AAACCTTGCCTGCTGTTCTCAGCGTGGCAACACAGATCACACGCGCTCTGCTCGGTGTGA 1020
Db 961 AAACCTTGCCTGCTGTTCTCGGCGTAGCAAAACAGATCACACGCGCTCTGCTCGGTGTGA 1020

QY 1021 AGCCACAGAGATCAGCATGCTTTTCTCACCGACTACATCAAGAGTGCCACCGGCTCTCAG 1080
Db 1021 AGCCACAGAGATCAGCATGCTTTTCTCACCGACTACATCAAGAGTGCCACCGGCTCTCAG 1080

QY 1081 TAATATTGCTCGGACAAAGAACGCGGCGAGTATATCGGATGCAAAACAGAGTGCCTG 1140
Db 1081 TAATATTGCTCGGACAAAGAACGCGGCGAGTATATCGGATGCAAAACAGAGTGCCTG 1140

QY 1141 CGGTGCTCTCTCAGTAGGGACTCGTTTCT-TAGTGGTCAATTCACAGGTATGCAGTTCGAT 1199
Db 1141 TGGTGTGCTCTCAGTGGGAGCTCGTTTCTCAAGTGGTCAATTCAGGTATGCAGTTCGAT 1200

QY 1200 TTGCCATGCCATGTCAAAGGAACCTTGTCCAGGCTCAGTGCACCTCAACACCCCGCTCGC 1259
Db 1201 TTGCCATGCCATGTCAAAGGAACCTTGTCCAGGCTCAGTGCACCTCAACACCCCGCTCGC 1260

QY 1260 TGGAAATTGAGCAGTCGCGGCTCCGGCTGTATAGTACGATCGGCTCGGGCGCGCTGTCG 1319
Db 1261 TGAATTTGAGCAGTCGCGCATCCGGCTGTACAGTACGATCGGCTCGGGCGCGCTGTCG 1320

QY 1320 AAGCAAAAAGTGTGGTTCGTTACCGACAATGTATCCCACTTGACATTTTCACC 1379
Db 1321 AAGCAAAAAGTGTGGTTCGTTACCGACAATGTATCCCACTTGACATTTTCACC 1380

QY 1380 ACCTCTTCCCGCGGAGAAAGCAATTTGGCGAAAATCTATCTCGGCTACTATAGCAA 1439
Db 1381 ACCCTCCCGCGGAGAAAGCAATTTGGCGAAAATTTCTATCTGGGCTACTATAGCAA 1440

QY 1440 GATAGTCTTGTATGGGACAAACCGGTGGCGGGAACAAAGGCTTCTCGGGCGCTCTCCA 1499
Db 1441 GATAGTCTTGTATGGGACAAACCGGTGGCGGGAACAAAGGCTTCTCGGGCGCTCTCCA 1500

QY 1500 ATCCAGCTGTGACCCCATCTCATTTGCCAGAGATACCAAGTATCGAATCGATCGCAATG 1559
Db 1501 ATCCAGCTGTGACCCCATCTCATTTGCCAGAGATACCAAGTATCGAATCGATCGCAATG 1560

QY 1560 GTCCATTACCTGTTTTCATGTCGGAGACCCGGGACCGGAAGTGGTCCCAACAGTCCAAAGCA 1619
Db 1561 GTCCATTACCTGTTTTCATGTCGGAGACCCGGGACCGGAAGTGGTCCCAACAGTCCAAAGCA 1620

QY 1620 GGTACGACAAAAGTCTGTCTGGGACCAACTCCGGCGAGCCTACGAGAACCCCGGGGCCCA 1679
Db 1621 GGTACGACAAAAGTCTGTCTGGGACCAACTCCGGCGAGCCTACGAGAACCCCGGGGCCCA 1680

QY 1680 AGTCCAGAGCCGGGCCAAACGTCGTAATTCGAAATCGAGTGGTCCGAAGCAGCATTTTCCAAGG 1739
Db 1681 AGTCCAGAGCCGGGCCAAACGTCGTAATTCGAAATCGAGTGGTCCGAAGCAGCATTTTCCAAGG 1740

QY 1740 AGCTCCGAGCGCGCTCTATGGGCTGAACAGATCTCATCACACTGGGTTTCGGCGCTCAGAAC 1799
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Db 1741 AGCTCCGAGCGCGTCTATGGGCTGACGATCTCATCACACTGGGTTCGGCGCTCAGAAC 1800
QY 1800 GCCGTTCAAGTGTGTCATTTCTGTTGGAACGGAGAGCTCTTTAGTTTGGAAAGGGTATAT 1859
Db 1801 GCCGTTCAAGAGTGTTCATTTCTGTTGGAACGGAGAGCTCTTTAGTTTGGAAAGGGTATAT 1860
QY 1860 GGAAGGGCCATAGATCGGTCACACGAGTGTGCGAGAGTTGTGGCTAGCCTGGTGCC 1919
Db 1861 GGAAGGGCCATAGATCGGTCACACGAGTGTGCGAGAGTTGTGGCTAGCCTGGTGCC 1920
QY 1920 AGCAGCATAG 1929
Db 1921 AGCAGCATAG 1930

RESULT 4

US-09-352-159-43
; Sequence 43, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
; APPLICANT: Duwick, Jonathan P.
; APPLICANT: Gulliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polylamine Oxidase
; TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
; FILE REFERENCE: 1134
; CURRENT APPLICATION NUMBER: US/09/352,159A
; EARLIER FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: 60/092,936
; EARLIER FILING DATE: 1998-07-25
; EARLIER APPLICATION NUMBER: 60/135,391
; EARLIER FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 43
; LENGTH: 1928
; TYPE: DNA
; ORGANISM: Rhinocliadiella atrovirens
; FEATURE:
; NAME/KEY: intron
; LOCATION: (739)...(811)
; NAME/KEY: intron
; LOCATION: (1134)...(1186)
US-09-352-159-43

Query Match 92.9%; Score 1792.2; DB 4; Length 1928;
Best Local Similarity 95.9%; Pred. No. 0;
Matches 1850; Conservative 0; Mismatches 78; Indels 1; Gaps 1;

QY 1 ATGGCAGCTTGACCGAGCTACATCAATCCCAACGTCGCTCCCAAGCAGGATATTC 60
Db 1 ATGGCAGCTTGACCGAGCTACATCAATCCCAACGTCGCTCCCAAGCAGGATATTC 60
QY 61 CACATCGGCTAGGCCCCAAACGAGGAGTGTGACAATAGCTGGACAGATTGGACAA 120
Db 61 TACGTCGGCGTAGGCCAAACGAGGAGGATGTGACAATAGCTGGACAGATTGGACAA 120
QY 121 GACGCTTTGGGCGTGACAGACCCAGCTACGAGAACAGGTTGCCAAGCATTCGCCAAT 180
Db 121 GACGCTTTGGGCGTGACAGACCCAGCTACGAGAACAGGTTGCCAAGCATTCGCCAAT 180
QY 181 CTGCGAGCTTGCTGTGCTGAGCTCTTCAACAGCAGCTCACCAAGCTCAATTTAC 240
Db 181 CTGCGAGCTTTGCTGTGCTGAGCTTTGAGCCACTTCAACAGCATTTACCAAGCTCAATTTAC 240
QY 241 TACATCGTCACTAGCCGCCAGCAAACTACCCGCAATTGGAGATGGGCTGAAGTCTACC 300
Db 241 TACATCGTCACTAGCAACCCGAGCAAACTACCCGCAATTGGAGATGGGCTGAAGGCTACC 300
QY 301 TTGCCCCCTTGACAGGCTCCCTCTTGCAGCTGGTGCCAGTACCGGCTTGCTTCACCT 360
Db 301 TTGCCCCCTTGACAGGCTCCCTCTTGCAGCTGGTGCCAGTACCGGCTTGCTTCACCT 360

QY 361 GAATACCTCTTTAGGTTGATGCCACGCGCTGGTGCCAGGACACTCGACCCCGAGACAAC 420
Db 361 GAATACCTCTTTAGGTTGATGCCACGCGCTGGTGCCAGGACACTCGACCCCGAGACAAT 420
QY 421 GTTGGCGAGCTGTAGTGGTGGGCGCTGGCTTGAGCGGTTTGGAGACGGCAGCAAGATC 480
Db 421 GTTGGCGAGCTGTGTGGTGGGCGCTGGCTTGAGCGGTTTGGAGACGGCAGCAAGATC 480
QY 481 CAGGCGCGCGGTCTGTCTCTGCTCGCTCTTGTGAGCGATGGATCGGTAGGGGGAAGACT 540
Db 481 CAGGCTGCGCGGTCTGTCTCTGCTCGCTCTTGTGAGCGATGGATCGGTAGGGGGAAGACT 540
QY 541 CTGAGCGTACAATCGGTCGCCGCGAGGAGCACTATCAACGACCTCGGGCGTGCGTGGATC 600
Db 541 CTGAGCGTACAATCGGTCGCCGCGAGGAGCACTATCAATGACCTCGGCGTGCGTGGATC 600
QY 601 AATGACGACCAACGAAGATATCCAGATTTGTTGAAAGATTTTCATTTGAGGGCGGAG 660
Db 601 AATGACGACCAACGAAGATATTCAAATTTATTTGAAAGATTTTCATTTGAGGGCGGAG 660
QY 661 CTCCAGAGCAGCAGCGGAAATTCATCCATCAAGCACAGACGGTACACCACTACAGCT 720
Db 661 CTCCAGAGCAGCAGCGGAAATTCATCCATCAAGCACAGACGGTACACCACTACAGCT 720
QY 721 CCTTATGTTGACTCCCGGTAAGCAATCCCACTTTGTGATGAGACCTCTCTCGAGTGT 780
Db 721 CCTTATGTTGATTCCTGTTAAGCAATTCATCTTGTGATGAGACCTCTCTCGTGTGT 780
QY 781 AGAATACAGTCACTGACTCCACTTGTCTGAGCTGAGCGAGGAGTTGCAAGTGCAGTTGC 840
Db 781 AGAATACAGTCACTGACTCCACTTGTCTGAGCTGAGCGAGGAGTTGCAAGTGCAGTGC 840
QY 841 GGAACCTCTCCCGTATGCTCTCAGCTGATCGAAGAGTATAGCTTGAAGACCCCAAGGC 900
Db 841 GGAACCTCTCCCGCATGCTCTCAGCTGATCGAAGAGCATAGTCTTGAAGACCCCAAGGC 900
QY 901 GAGCCCTCAGCGAAGCGCTGCACAGTGTGAGCTTTCGCGCACACTACTGTGAGAAGSACT 960
Db 901 GAGCCCTCAGCGAAGCAGCTGCACAGTGTGAGCTTTCGCGCACACTACTGTGAGAAGSACT 960
QY 961 AAACCTGCGTGTGTTCTCAGCGTGCAACACAGATCACACGGCTCTCTCGGTGTGGA 1020
Db 961 AAACCTGCGTGTGTTCTCGCGTGCAACACAGATCACACGGCTCTCTCGGTGTGGA 1020
QY 1021 AGCCACGAGATCAGCATGCTTTTCTCAGCGACTACTACAGAGTGCACCGGTCTCAG 1080
Db 1021 AGCCACGAGATCAGCATGCTTTTCTCAGCGACTACTACAGAGTGCACCGGTCTCAG 1080
QY 1081 TAATATTGCTCGGACAAAGAACGCGGCGGAGTATATCGGATGCAAAACAGGTGCGGTG 1140
Db 1081 TAATATTGCTCGGATAAAGAACGCGTGGCGAGTATATCGGATGCAAAACAGGTGCGGTG 1140
QY 1141 CGGTGCTCTCAGTAGGAGTCTGTTTCTAGTGTCTATTCAGTATCCAGTATGCAAGTAT 1200
Db 1141 TGGTGTCTCTCA-GTGGGAGACTCGTTTCTTAGTGTCTATTCAGTATGCAAGTATGCA 1199
QY 1201 TGCCATGCCATGTCAAAGGAACTTGTTCAGGCTCAGTGCACCTCAACACCCCGCTCGCT 1260
Db 1200 TGCCATGCCATGTCAAAGGAACTTGTTCAGGCTCAGTGCACCTCAACACCCCGCTCGCC 1259
QY 1261 GGAATTGAGCAGTCCGCGTCCGCTGTATAGTACGATCGGCGCTCGGGCGGCTGTTCCGA 1320
Db 1260 GAAATTGAGCAGTCCGCGTCCGCTGTATAGTACGATCGGCGCTCGGGCGGCTGTTCCGA 1319
QY 1321 AGCAAAAGTGTGTTTCTGTTACCGACACATTTGATCCACCTTGACATTTTCACCA 1380
Db 1320 AGTAAAAAGTGTGTTTCTGTTACCGACACATTTGATCCACCTTGATATTTTCACCA 1379
QY 1381 CCTCTTCCCGCCGAGAACGATTTGGCGGAAAAATCTATCTCTCGGCTACTATAGCAAG 1440
Db 1380 CCTCTTCCCGCCGAGAACGATTTGGCTGAAAAATCCATCTCTGGGCTACTATAGCAAG 1439

| | | | |
|------|--|--|------|
| QY | 1441 | ATAGTCTTCGTATGGGACAACCCGGTGGCCGCGCAACAGGCTTCTCGGGCGCTCCTCAA | 1500 |
| Db | | | |
| 1440 | ATAGTCTTCGTATGGGACAACCCGGTGGCCGCGCAACAGGCTTCTCGGGCGCTCCTCAA | 1499 | |
| QY | 1501 | TCGAGCTGTGACCCCATCTCATTTGCCAGAGATACACAGATCGAAGTCGATCGGAATGG | 1560 |
| Db | | | |
| 1500 | TCGAGCTGTGACCCCATCTCATTTGCCAGAGATACACAGATCGAAGTCGATCGGAATGG | 1559 | |
| QY | 1561 | TCCAATTACCTGTTTCATGTGTCGAGACCCGGGACGGAAGTGGTCCCAACAGTCCCAAGCAG | 1620 |
| Db | | | |
| 1560 | TCCAATTACCTGTTTCATGTGTCGAGACCCGGGACGGAAGTGGTCCCAACAGTCCCAAGCAG | 1619 | |
| QY | 1621 | GTACGACAAAAGTCTGTCTGGGACCAACTCCGCGCAGCGCTACGAGAACGCCGGGGGCCCAA | 1680 |
| Db | | | |
| 1620 | GTACGACAGAAGTCTGTCTGGAACCAACTCCGCGCAGCGCTACGAGAACGCCGGGGGCCCAA | 1679 | |
| QY | 1681 | GTCCAGAGCGCGGCAACGTCGCTGAAATCGAGTGGTGAAGCAGCAGTATTTCCAAAGGA | 1740 |
| Db | | | |
| 1680 | GTCCAGAGCGCGGCAACGTCGCTGAGATCGAGTGGTGAAGCAGCAGTATTTCCAAAGGA | 1739 | |
| QY | 1741 | GGTCGAGCGCGCTATGTGGGCTGAACCATCTCATCACACTGGGTTCCGGCGCTCAGAACG | 1800 |
| Db | | | |
| 1740 | GGCGCGAGCGCGCTATGTGGGCTGAACCTCTCAACACACTGGGTTCCGGCGCTCAGAACG | 1799 | |
| QY | 1801 | CGGTTCAAGTGTGTTCAATTCGTTGGAAACGAGAGCGTCTTTAGTTTGGAAAGGGTATATG | 1860 |
| Db | | | |
| 1800 | CGGTTCAAGGGTGTTCATTTTCGTTGGAACGAGAGCGTCTTTGGTTTGGAAAGGGTATATG | 1859 | |
| QY | 1861 | GAAGGGGCCATACGATCGGCTCAACGAGGTGCTCGAAGAGTTGTGGCTAGCCTGGTGCCA | 1920 |
| Db | | | |
| 1860 | GAAGGGGCCATACGATCGGCTCAGCGAGGCGCTGCAGAAAGTTGTGGCTAGCCTGGTGCCA | 1919 | |
| QY | 1921 | GCAGCATAG 1929 | |
| Db | | | |
| 1920 | GCAGCATAG 1928 | | |

RESULT 5

US-09-352-159-45

; Sequence 45, Application US/09352159A

; Patent No. 6211434

; GENERAL INFORMATION:

; APPLICANT: Duwick, Jonathan P.

; APPLICANT: Gilliam, Jacob T.

; APPLICANT: Maddox, Joyce R.

; TITLE OF INVENTION: Amino Polylamine Oxidase

; TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use

; FILE REFERENCE: 1134

; CURRENT APPLICATION NUMBER: US/09/352,159A

; CURRENT FILING DATE: 1999-07-12

; EARLIER APPLICATION NUMBER: 60/092,936

; EARLIER FILING DATE: 1998-07-25

; EARLIER APPLICATION NUMBER: 60/135,391

; EARLIER FILING DATE: 1999-05-21

; NUMBER OF SEQ ID NOS: 46

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 45

; LENGTH: 1928

; TYPE: DNA

; ORGANISM: Rhinocladia atrovirens

; FEATURE:

; NAME/KEY: intron

; LOCATION: (739)...(811)

; NAME/KEY: intron

; LOCATION: (1134)...(1185)

US-09-352-159-45

Query Match 92.7%; Score 1789; DB 4; Length 1928;

Best Local Similarity 95.8%; Pred.No. 0;

Matches 1848; Conservative 0; Mismatches 80; Indels 1; Gaps 1;

| | | | |
|----|---|--|----|
| QY | 1 | ATGCACCTTCACCGAGCTACATCATCCCCAAAGCTCCGCCCTCCCCAGCAGGGAATTC | 60 |
| | | | |

| | | | |
|----|------|---|------|
| Db | 1 | ATGCGACTTTGCACCGGAGCTACATCAATCCCCTCCAAACCTCGCTCCCTCCAGCAGGGTATTCC | 60 |
| QY | 61 | CACATCGGGCTAGGCCCAAGAGCGAGGTATGTGACAAATAGCTGGACAGATTGGACAA | 120 |
| Db | 61 | CACGTCCGGCTAGGCCCAAGAGCGAGGGTATGTGACAAATAGCTGGACAGATTGGACAA | 120 |
| QY | 121 | GAGGCTTTGGGCGTCACAGACCCAGCCTACAGAGAAACAGGTTGCCCAAGCATTCGCGCAAT | 180 |
| Db | 121 | GAGCGTTCGGCGCTGACAGACCTTCCTTACAGAGAAACAGGTTGCCCAAGCATTCGCGCAAC | 180 |
| QY | 181 | CTCGAGCTTGCTTTGCTGCAGTTGGAGCCCTCTTCAACGACGCTACCAAGCTCAATTAC | 240 |
| Db | 181 | CTCGAGCTTGCTTTGCTGCAGTTGGAGCCCACTTCAACGACATTCACCAAGCTCAATTAC | 240 |
| QY | 241 | TACATGTGCACTAGCCGCCGAGCAAACTCACCGCAATTGGAGATGGCTGAAAGTCTACC | 300 |
| Db | 241 | TACATCGTGCAGCTACAACCCGAGCAAACTCACCGCAATTGGAGATGGCTGAAAGCTACC | 300 |
| QY | 301 | TTTGCCCTTGACAGGCTCCCTCCTTGTGACGCTGCTGCCAGTACGGGCTTGGCTTCACCT | 360 |
| Db | 301 | TTTGCCCTTGACAGGCTCCCTCCTTGTGACGCTGCTGCCAGTACGGGCTTGGCTTCACCT | 360 |
| QY | 361 | GAATACCTCTTTGAGTTGATGCCACGGCGTGTGCCAGGACACTCGACCCAGACAAC | 420 |
| Db | 361 | GAATACCTCTTTGAGTTGATGCTACGGCGTGTGCCAGGACACTCAACCCAGACAAT | 420 |
| QY | 421 | CTTCGGGAGCTGTAGTGGTGGGCGCTGGCTTGAGCGGTTTGAGACGGCAGCAAAAGTC | 480 |
| Db | 421 | GTTCGGGAGCTGTGTGGTGGGCGCTGGCTTGAGCGGTTTGAGACGGCAGCAAAAGTC | 480 |
| QY | 481 | CAGGCGCGCGGTCTGCTCCTGCCTCGTTCTTGAGCGGATGATCGTGTAGGGGGAAGACT | 540 |
| Db | 481 | CAGGCTCGCGGGCTCTGCTCCTCGTTCTTGAGCGGATGATCGTGTAGGGGGAAGACT | 540 |
| QY | 541 | CTGAGCGTACAATCGGGTCCGGCAGGACGACTATCAACGACCTCGCGCTCGCTGGATC | 600 |
| Db | 541 | CTGAGCGTACAATCGGGTCCGGCAGGACGACTATCAATGACCTCGCGCTCGCTGGATC | 600 |
| QY | 601 | AATGACACCAACCAAGCGAGTATCCAGATTGTTGAAAGATTTCATTTGAGGGCGGAG | 660 |
| Db | 601 | AATGACACCAACCAAGCGGAATTCAAAATATTTGAAAGATTTCATTTGAGGGCGGAG | 660 |
| QY | 661 | CTCCAGAGGAGCGCGGAAATTCATCCATCAAGCAACAGCGGTACACCACTACAGCT | 720 |
| Db | 661 | CTCCAGAGGAGCGCGGAATTCATCCATCAAGCAACAGCGGTACACCACTACAGCT | 720 |
| QY | 721 | CGTTATGTGACTCCCGGTAAAGCAATCCCACCTTTGTGATGAGACCTCTCTCGAGTGT | 780 |
| Db | 721 | CGTTATGTGATTCCCTGGTAGGCACAATTCCTACTTGTGATGAGACCTCTCTCGTGTGT | 780 |
| QY | 781 | AGAAATACAGTCACTTCCACTTCGTCAGCTGAGCGGAGGTTGCAAGTGCACCTTGC | 840 |
| Db | 781 | AGAAATACAGTCCGCTGACTCCACATCGTCCAGCTGAGCGGAGGTTGCAAGTGCACCTGC | 840 |
| QY | 841 | GGAACCTCCTCCCGGTATGGTCTCAGCTGATCGAAGAGTATAGCCTTTGAAGACCCCAAGGC | 900 |
| Db | 841 | GGAACCTCCTCCCGCATGGTCTCAGCTGATCGAAGAGTATAGTCTTGAGACCCCAAGGC | 900 |
| QY | 901 | GAGCCCTAGCGGAAGCGGCTGCACAGTGTGAGCTTCGCGCACTACTGTGAGAAGGACT | 960 |
| Db | 901 | GAGCCCTCAAGCGAAGCAGCTCGACAGTGTGAGCTTCGCACTACTGTGAGAAGGACT | 960 |
| QY | 961 | AAACTTGCCTGCTTCTCAGCGTGGCAACCAAGATCACACGGCTCTGCTCGGTGTGGA | 1020 |
| Db | 961 | AAACTTGCCTGCTTCTCAGCGTGGCAACCAAGATCACACGGCTCTGCTCGGTGTGGA | 1020 |
| QY | 1021 | AGCCCCAGGATCAGCATGCTTTTCTCACCGACTACATCAAGAGTGCACCGGTCTCAG | 1080 |
| Db | 1021 | AGCCCCAGGATCAGCATGCTTTTCTCACCGACTACATCAAGAGTGCACCGGTCTCAG | 1080 |
| QY | 1081 | TAATATTGCTCGCACAAAGAACGCGGGCGGAGTATATGCGATGCAAAACAGGTGCGTG | 1140 |
| Db | 1081 | TAATATTGCTCGGATTAAGAAACGCGTGGGAGTATATGCGATGCAAAACAGGTGCGTG | 1140 |

| | | | |
|----|------|---|------|
| Db | 781 | AGAATACAGTCGCTGACTCCACATCTCCAGTCGAGCGAGGAGGTTGCAAGTGCACCTCGC | 840 |
| QY | 841 | GGAACTCTCCCCGATGTGCTCAGCTGATCGAAGAGTATAGCTTTGAAGACCCCAAGGC | 900 |
| Db | 841 | GGAACTCTCTCCGCGATGGTCTCAGCTGATCGAAGAGCATAGTCTTGAAGACCCCAAGGC | 900 |
| QY | 901 | GAGCCCTCAGCGAAGCGGCTCGACAGTGTGAGCTTCCGCGCACTACTGTGAGAGGACCT | 960 |
| Db | 901 | GAGCCCTCAAGCGAAGCAGCTCGACAGTGTGAGCTTCGCACTACTGTGAGAGGATCT | 960 |
| QY | 961 | AAACTTGGCTCTCTTCAGGCTGGCAAAACAGATCACACGCGCTCTCTCGTGTGGA | 1020 |
| Db | 961 | AACTTGGCTCTCTTCGCGGTGCAAAACAGATCACACGCGCTCTCTCGTGTGGA | 1020 |
| QY | 1021 | AGCCCAACAGATCAGATCTTTCTCACCAGTACTCATCAAGTAGCCACCGGCTCTCAG | 1080 |
| Db | 1021 | AGCCCAAGAGATCAGATCTTTCTCACCAGTACTCATCAAGTGTCCACCGGCTCTCAG | 1080 |
| QY | 1081 | TAATATTCTCTCGACAAAGAGGCGGCGAGTATATCGATCGAAACAGGTGCGTG | 1140 |
| Db | 1081 | TAATATTCTCTCGATAAGAAACGCGTGGCGAGTATATCGATCGAAACAGGTGCGTG | 1140 |
| QY | 1141 | CGGTGCTCTCAGGTAGGGAGCTCGTTTCTTGTGTGTCATTCAGGTATGCAGTCGATT | 1200 |
| Db | 1141 | TGGTGTCTCTCA-CTGGGAGACTCGTTTCTTGTGTGTCATTCAGGTATGCAGTCGCTT | 1199 |
| QY | 1201 | TGCCATGCCATGTCAAAGAACCTGTTTCCAGGCTCAGTGCACTCAACACCCCGTCGCT | 1260 |
| Db | 1200 | TGCCATGCCATGTCAAAGAACCTGTTTCCAGGCTCAGTGCACTCAACACCCCGTCGCT | 1259 |
| QY | 1261 | GGAATTGAGCAGTCGGCGTCCGGCTGATATAGTAGCATCGGCTCGGGCGCGTGTCCGA | 1320 |
| Db | 1260 | GAAATTGAGCAGTCGGCATCCGGCTGACAGTAGCATCGGCTCGGGCGCGTGTCCGA | 1319 |
| QY | 1321 | ACAAAAAGTGTGTTTCGTTTACCGACACATGTATCCCACTTGACATTTTCACCA | 1380 |
| Db | 1320 | AGTAAAAAGTGTGTTTCGTTTACCGACACCTGTATCCCACTTGATATTTTCACCA | 1379 |
| QY | 1381 | CTCTTCCCGCGGAGAAGCAAGATTGGGGAAAATCTATCTCGCTGCTACTATAGCAAG | 1440 |
| Db | 1380 | CCTCTTCCCGCGGAGAAGCAAGATTGGCTGNAAATCCCATCTCGGCTACTATAGCAAG | 1439 |
| QY | 1441 | ATAGTCTTCTGATGGGACAACCGGTGTGGCGCGGAGCAAGGCTTCTCGGGCGTCTCCAA | 1500 |
| Db | 1440 | ATAGTCTTCTGATGGGACAACCGGTGTGGCGGCAAGGCTTCTCGGGCGTCTCCAA | 1499 |
| QY | 1501 | TCGAGCTGTGACCCCATCTCATTTGCCAGAGATACCAAGTCTGAAAGTCGATCGGCAATGG | 1560 |
| Db | 1500 | TCGAGCTGTGACCCCATCTCATTTGCCAGAGATACCAAGTCTGAAAGTCGATCGGCAATGG | 1559 |
| QY | 1561 | TGCATTACTGTTCATGTGCGAGACCGCGGAGCGGAGTGTTCACACAGTCTCAAGCAG | 1620 |
| Db | 1560 | TGCATTACTGTTCATGTGCGAGACCGCGGAGCGGAGTGTTCACACAGTCTCAAGCAG | 1619 |
| QY | 1621 | GTACGACAAAAGTCTGTCTGGGACCAACTCCGCGCAGCTACGAGAACCCCGGGGCCCAA | 1680 |
| Db | 1620 | GTACGACAAAGTCTGTCTGGAACCAACTCCGCGCAGCTACGAGAACCCCGGGGCCCAA | 1679 |
| QY | 1681 | GTCCAGAGCGGCCCAACGTCGTAATTCGAGTGTTCGAGCAGCAGTATTTCCAGGA | 1740 |
| Db | 1680 | GTCCAGAGCGGCCCAACGTCGTAATTCGAGTGTTCGAGCAGCAGTATTTCCAGGA | 1739 |
| QY | 1741 | GTCTCGAGCGCGTCTATGCGCTGAACGATCTCATCTACCTGGGTCGCGCTCAGAAGC | 1800 |
| Db | 1740 | GGCGCGAGCGTCGTATGCGCTGAACCTGTCTCAACACACTGGGTCGCGCTCAGAAGC | 1799 |
| QY | 1801 | CGTTCAGTGTGTCATTTCGTGTGCAAGGAGCGTCTTATGTTTGGAAAGGTTATATG | 1860 |
| Db | 1800 | CGTTCAGAGGTGTTCAATTTCGTGTGACGAGAGCTCTTTGGTTTGGAAAGGTTATATG | 1859 |
| QY | 1861 | GAAGGGCCATACGATCCGGTCAAGCGGTGCTCGAAGAGTCTGGCTAGCCTGGTGCCA | 1920 |
| Db | 1860 | GAAGGGCCATACCATCCGCTCAGCAGCGCTGCAAGTGTGGCTAGCCTGGTGCCA | 1919 |

| | | | |
|----|------|-----------|------|
| Qy | 1921 | GCAGCATAG | 1929 |
| | | | |
| Db | 1920 | GCAGCATAG | 1928 |

RESULT 7

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US-09-352-159-22
; Sequence 22, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
; APPLICANT: Duwick, Jonathan P.
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
; FILE REFERENCE: 1134
; CURRENT APPLICATION NUMBER: US/09/352,159A
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: 60/092,936
; EARLIER FILING DATE: 1998-07-25
; EARLIER APPLICATION NUMBER: 60/135,391
; EARLIER FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 1803
; TYPE: DNA
; ORGANISM: Exophiala spinifera
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1800)
US-09-352-159-22

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Query Match 83.1%; Score 1602.6; DB 4; Length 1803;
Best Local Similarity 91.7%; Pred. NO. 0;
Matches 1769; Conservative 0; Mismatches 34; Indels 126;

| | | | |
|----|-----|--|-----|
| Qy | 1 | ATGGCACTTGCACCGAGCTACATCAATCCCCAAACGTCGCTCCCCAGCAGGATATTC | 60 |
| Db | 1 | ATGGCACTTGCACCGAGCTACATCAATCCCCAAACGTCGCTCCCCAGCAGGATATTC | 60 |
| Qy | 61 | CACATCGCGGTAGGCGCCAAACGAACGAGCGAGTATGTGACAAATAGCTGGACAGATTGGACAA | 120 |
| Db | 61 | CACGTCGCGGTAGGCGCCAGACGGAGGGAGGTATGTGACAAATAGCTGGACAGATTGGACAA | 120 |
| Qy | 121 | GAGCTTTTGGGCGTGACAGACCCAGCCTACGAGAAACAGGTTGCCAAGCAATTCGCCAAT | 180 |
| Db | 121 | GAGCGCTTGGGCGTGACAGACCCCTGCTACGAGAAACAGGTTGCCAAGCAATTCGCCAAT | 180 |
| Qy | 181 | CTGCGAGCTTGGCTTGTCTGTCAGTTGGAGCGCTCTTAAACGAGCGTCACCACAGCTCAATTTAC | 240 |
| Db | 181 | CTGCGAGCTTGGCTTGTCTGTCAGTTGGAGCGCCATCTCAACGAGCGTCACCACAGCTCAATTTAC | 240 |
| Qy | 241 | TACATCGTCGACTAGCGCCCCGAGCAAACTCACCGCAATTTGGAGATGGGCTGAAGCTTACC | 300 |
| Db | 241 | TACATCGTCGACTAGCGCCCCGAGCAAACTCACCGCAATTTGGAGATGGGCTGAAGGCTTACC | 300 |
| Qy | 301 | TTTGGCCCTTGACAGAGCTCCCTTCCTTGACAGCTGGTCGCCAGTACCGGGCTTGGCTTACCT | 360 |
| Db | 301 | TTTGGCCCTTGACAGAGCTCCCTTCCTTGACAGCTGGTCGCCAGTCTCGGCCCTTGTCTTACCT | 360 |
| Qy | 361 | GAATACCTCTTTGAGTTGTATGCAACGGCGCTGGTCCCGAGCACACTCGACCCCCAGACAAC | 420 |
| Db | 361 | GAATACCTCTTTGAGTTGTATGATCCACGGCGCTGGTCCCGGAGACACACGCCCCCCAGACAAC | 420 |
| Qy | 421 | GTTTGGGACGCTGATAGTGGGCGCTGGCTTCAGCGGTTTGGACAGCGCACGCAAAAGTC | 480 |
| Db | 421 | GTTTGGGACGCTGATAGTGGGCGCTGGCTTCAGCGGTTTGGACAGCGCACGCAAAAGTC | 480 |
| Qy | 481 | CAGCGCGCGGCTCTCTCTGCTCTTTGAGCGCATGGATCGTGTAGGGGGGAAAGACT | 540 |
| Db | 481 | CAGCGCGCGGCTCTCTCTGCTCTTTGAGCGCATGGATCGTGTAGGGGGGAAAGACT | 540 |


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QY 241 TACATCGTCGACTACGCCCGGAGCAAACTCACCGCAATTGGAGATGGGCTGAAGTCTACC 300
Db 241 TACATCGTCGACTACGCCCGGAGCAAACTCACCGCAATTGGAGATGGGCTGAAGGCTACC 300
QY 301 TTTCGCCCTTGACAGGCTCCCTCTCTTGACCGCTGGTGCACGTACCGGCGCTTGGGCTTCACCT 360
Db 301 TTTCGCCCTTGACAGGCTCCCTCTCTTGACCGCTGGTGCACGTACCGGCGCTTGGGCTTCACCT 360
QY 361 GAATACCTCTTTGAGGTGATGCCACCGCGCTGGTGCAGGACACTCGACCCCGAGCAAC 420
Db 361 GAATACCTCTTTGAGGTGATGCCACCGCGCTGGTGCAGGACACTCGACCCCGAGCAAC 420
QY 421 GTTCGGGACGTGGTAGTGGGCGCTGGCTTGAGCGGTTTGGAGACGGCAGCAAAAGTC 480
Db 421 GTTCGGGACGTGGTAGTGGGCGCTGGCTTGAGCGGTTTGGAGACGGCAGCAAAAGTC 480
QY 481 CAGCGCCCGGCTGTGCTCCCTCGCTTCTTGAGCGGATGGATCGTGTAGGGGGAAGACT 540
Db 481 CAGCGCCCGGCTGTGCTCCCTCGCTTCTTGAGCGGATGGATCGTGTAGGGGGAAGACT 540
QY 541 CTGAGCGTACAATCGGCTCCCGGAGGACACTATCAAGGACCTCGGCGCTGGCTGGATC 600
Db 541 CTGAGCGTACAATCGGCTCCCGGAGGACACTATCAAGGACCTCGGCGCTGGCTGGATC 600
QY 601 AATGACAGCAACCAAGCGAAGTATCCAGATTGCTTTGAAAGATTTCATTTGGAGGCGAG 660
Db 601 AATGACAGCAACCAAGCGAAGTATCCAGATTGCTTTGAAAGATTTCATTTGGAGGCGAG 660
QY 661 CTCAGAGGACGACCGGAAATTCATCCATCAAGCAACAAGCGGTACAACCACTACAGCT 720
Db 661 CTCAGAGGACGACCGGAAATTCATCCATCAAGCAACAAGCGGTACAACCACTACAGCT 720
QY 721 CTTATGGTGACTCCCGGCTAAGCAATCCACATTTGTGATGAGACCTCTCTCGAGTGT 780
Db 721 CTTATGGTGACTC----- 734
QY 781 AGAATACAGTCACTGACTCCACTTCCTCCAGCTGACGAGGAGGTTGCAAGTGCAGTTGC 840
Db 735 -----CTGTGTGAGCGAGGAGGTTGCAAGTGCAGTTGC 767
QY 841 GGAACCTCCTCCCGTATGTCTCAGCTGATCGAAGAGTATAGCCTTGAAGACCCCAAGC 900
Db 768 GGAACCTCCTCCCGTATGTCTCAGCTGATCGAAGAGTATAGCCTTGAAGACCTCAAGGC 827
QY 901 GAGCCCTCAGGCGAAGCGGCTCGACAGTGTGAGCTTCGCGCACTACTGTGGAAGAACT 960
Db 828 GAGCCCTCAGGCGAAGCGGCTCGACAGTGTGAGCTTCGCGCACTACTGTGGAAGAACT 887
QY 961 AAACCTTCCTGTGTCTCAGCGTGGCAAAACAGATCACACGCGCTCTGCTGGGTGGA 1020
Db 888 AAACCTTCCTGTGTCTCAGCGGTAGCAAAACAGATCACACGCGCTCTGCTGGGTGGA 947
QY 1021 AGCCACAGAGTACAGATGCTTTTCTACCGACTACATCAAGAGTGCACCGGTCTCAG 1080
Db 948 AGCCACAGAGTACAGATGCTTTTCTACCGACTACATCAAGAGTGCACCGGTCTCAG 1007
QY 1081 TAATATTGCTCGGCAAGAGCGGCGGAGTATATGCGATCAAAACAGGTGCGTG 1140
Db 1008 TAATATTCTCGGCAAGAGCGGCGGAGTATATGCGATCAAAA----- 1057
QY 1141 CGGTGCTCTCTCAGGTAGGGGACTCGTCTTCTAGTGGTCAATTCAGGTATGAGTCGATT 1200
Db 1058 -----CAGGTATGAGTCGATT 1074
QY 1201 TGCCATGCATGCAAGGAAGCTTTGTCAGGCTCAGTGCACCTCAACACCCCGCTGCT 1260
Db 1075 TGCCATGCATGCAAGGAAGCTTTGTCAGGCTCAGTGCACCTCAACACCCCGCTGCT 1134
QY 1261 GGAATTGAGCAGTGGCGCTCGGCTGTATGATGAGTACGCGCTCGGGCGCGGTTCGGA 1320
Db 1135 GAAATTGAGCAGTGGCGCTCGGCTGTATGATGAGTACGCGCTCGGGCGCGGTTCGGA 1194
QY 1321 AGCAAAAAAGGTGGTGGTTTTCGTTACCGCAACAATTGTATCCCACTTGCACATTTTCACCA 1380
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Db 1195 ACARAAAAGTGGTGGTTTCGTTACCGAACCTTGTATCCACCTTGACATTTTCACCA 1254
QY 1381 CCTCTTCCCGCCGAGAAGCAAGCATTTGGCGGAAAAATCTATCCTCGGCTACTATAGCAAG 1440
Db 1255 CCTCTTCCCGCCGAGAAGCAAGCATTTGGCGGAAAAATCTATCCTCGGCTACTATAGCAAG 1314
QY 1441 ATAGTCTTCGTATGGGCAACACCCGTTGGCGGCAAGGCTTCTCGGGGCTCCTCAA 1500
Db 1315 ATAGTCTTCGTATGGGCAAGCCGTTGGCGGCAAGGCTTCTCGGGGCTCCTCAA 1374
QY 1501 TCGAGCTGTGACCCCTCTCATTTGCCAGAGATACCAACATCGAAGTCGATCGCAATGG 1560
Db 1375 TCGAGCTGTGACCCCTCTCATTTGCCAGAGATACCAACATCGAAGTCGATCGCAATGG 1434
QY 1561 TCATTACTGTGTTTCATGGTGGAGACCCGGGACGAAAGTGTCCCAACAGTCCCAAGCAG 1620
Db 1435 TCATTACTGTGTTTCATGGTGGAGACCCGGGACGAAAGTGTCCCAACAGTCCCAAGCAG 1494
QY 1621 GTACGACAAAAGTCTCTGGGACCAACTCCGCGCAGCTACGAGAACGCCGGGGCCAA 1680
Db 1495 GTACGACAAAAGTCTCTGGGACCAACTCCGCGCAGCTACGAGAACGCCGGGGCCAA 1554
QY 1681 GTCCAGAGCCGCGCAACGCTCTGAAATCGAGTGGTGAAGCAGCAGTATTTCCAAAGGA 1740
Db 1555 GTCCAGAGCCGCGCAACGCTCTGAAATCGAGTGGTGAAGCAGCAGTATTTCCAAAGGA 1614
QY 1741 GCTCGAGCGCGCTCTATGGGCTGAACGATCTCATACACTGGGTTCCGGGCTCAGAAGC 1800
Db 1615 GCTCGAGCGCGCTCTATGGGCTGAACGATCTCATACACTGGGTTCCGGGCTCAGAAGC 1674
QY 1801 CCGTTCAAGTGTGTTCATTCTGTTGGAACGAGAGCGCTTTAGTTTGAAGGTTATATG 1860
Db 1675 CCGTTCAAGTGTGTTCATTCTGTTGGAACGAGAGCGCTTTAGTTTGAAGGTTATATG 1734
QY 1861 GAAGGGCCATACGATCGGTCACAGAGGTGCTCGAGAAGTTGTGGCTAGCCTGGTGCCA 1920
Db 1735 GAAGGGCCATACGATCGGTCACAGAGGTGCTCGAGAAGTTGTGGCTAGCCTGGTGCCA 1794
QY 1921 GCAGCATAG 1929
Db 1795 GCAGCATAG 1803

RESULT 9
US-09-352-159-32
; Sequence 32, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
; APPLICANT: Duwick, Jonathan P.
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
; FILE REFERENCE: 1134
; CURRENT APPLICATION NUMBER: US/09/352,159A
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: 60/092,936
; EARLIER FILING DATE: 1998-07-25
; EARLIER APPLICATION NUMBER: 60/135,391
; EARLIER FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 2490
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: GST:glyc(-)APAO open reading frame, 2490 nt; GST
; OTHER INFORMATION: and linker, nt 1-687; glyc (-) APAO, nt 688-2490;
; OTHER INFORMATION: mutation in putative glycosylation sites, nt
; OTHER INFORMATION: 1288-1290 (AAT-> TCC) and nt 1303-1305 (AGC->AAC).
; FEATURE:
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; NAME/KEY: CDS
; LOCATION: (1)...(2487)
; NAME/KEY: misc_feature
; LOCATION: (1)...(687)
; OTHER INFORMATION: GST and linker
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (688)...(2490)
; OTHER INFORMATION: Glyc (-) APAO
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (1288)...(1290)
; OTHER INFORMATION: mutation in putative glycosylation site (AAT->TCC)
; FEATURE:
; NAME/KEY: mutation
; LOCATION: (1303)...(1305)
; OTHER INFORMATION: mutation in putative silycosylation site (AGC->AAC)
; US-09-352-159-32

Query Match      82.7%; Score 1596.2; DB 4; Length 2490;
Best Local Similarity 91.5%; Pred. No. 0;
Matches 1765; Conservative 0; Mismatches 38; Indels 126; Gaps 2;

QY 1 ATGCGACCTTGACCGAGCTACATCAATCCCCAAAGCTGCGCTCCCCAGCAGGGTATTC 60
DB 688 ATGCGACCTTGACCGAGCTACATCAATCCCCAAAGCTGCGCTCCCCAGCAGGGTATTC 747
QY 61 CACATCGGGTAGGCCCAACAGAGCGAGGTATGTGACATAGCTGGACAGATGGACAA 120
DB 748 CACATCGGGTAGGCCCAACAGAGCGAGGTATGTGACATAGCTGGACAGATGGACAA 807
QY 121 GACGCTTTGGCGNGACAGACCCAGCGCTACGAGAAACAGGTTGCCAAAGCATTCGCCAAT 180
DB 808 GACGCTTTGGCGGTGACAGACCCCTGCTGACGAGAAACAGGTTGCCAAAGCATTCGCCAAT 867
QY 181 CTGGAGGCTTGCCCTTGCTGACGTTGGAGCCTCTTCAACAGACGTCAACAGCTCAATTAC 240
DB 868 CTGGAGGCTTGCCCTTGCTGACGTTGGAGCCTCTTCAACAGACGTCAACAGCTCAATTAC 927
QY 241 TACATCGTCGACTACGCCCGGAGCAAACTCACGCCAATTTGGAGATGGCTGAAGTCTACC 300
DB 928 TACATCGTCGACTACGCCCGGAGCAAACTCACGCCAATTTGGAGATGGCTGAAGTCTACC 987
QY -301 TTTGCCCTTGACAGGCTCCCTCCCTTGACGCTGGTGCCAGTACCGGCTTGGCTTCACCT 360
DB 988 TTTGCCCTTGACAGGCTCCCTCCCTTGACGCTGGTGCCAGTACCGGCTTGGCTTCACCT 1047
QY 361 GAATACCTCTTTGAGTTGATGCGACGCGCTGTCGCGAGACACTCGACCCAGACAAC 420
DB 1048 GAATACCTCTTTGAGTTGATGCGACGCGCTGTCGCGGAGACACAGACCCAGACAAC 1107
QY 421 GTTGGGACGTTGAGTGGTGGCGCTGGCTTGAGCGGTTTGGAGCGGCGACGCAAAAGTC 480
DB 1108 GTTGGGACGTTGAGTGGTGGCGCTGGCTTGAGCGGTTTGGAGCGGCGACGCAAAAGTC 1167
QY 481 CAGGCGCGGCTGCTGCTGCTGCTGCTTGGAGCGATGGATCGTGTAGGGGGAAAGACT 540
DB 1168 CAGGCGCGGCTGCTGCTGCTGCTGCTTGGAGCGATGGATCGTGTAGGGGGAAAGACT 1227
QY 541 CTGACGCTACATCGGGTCCCGGAGGACGACTATCAACGACCTTCGGGCTCGCGTGATC 600
DB 1228 CTGACGCTACATCGGGTCCCGGAGGACGACTATCAACGACCTTCGGGCTCGCGTGATC 1287
QY 601 AATGACACCAACCAAGCAAGTATCCAGATTTTGAAGATTTTCAATTTGGAGGGCGAG 660
DB 1288 TCCGACAGCAACCAAAAGCAAGTATCCAGATTTTGAAGATTTTCAATTTGGAGGGCGAG 1347
QY 661 CTCCAGAGACGACCGGAAATTCATTCATCAAGCACAAAGACGGTACAAACACTACAGCT 720
DB 1348 CTCGAGAGGACGACTGGAATTCATTCATCAAGCACAAAGACGGTACAAACACTACAGCT 1407
QY 721 CTTTATGTTGACTCCCGGTGAAGCAATCCCACTTTGTGTGATGAGACCTCTGTCTGAGTGT 780
      |||||||
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DB 1408 CCTTATGGTGACTC----- 1421
QY 781 AGAATACAGTCACTGACTCCACTTCGCTCCAGCTGAGCGAGAGGTTGCAAGTGCACCTTGC 840
DB 1422 -----CTTGCTGAGCGAGGAGGTTGCAAGTGCACCTTGC 1454
QY 841 GGAATCCTCCCGTATGGTCTCAGCTGATCGAAGAGTATAGCCTTGAAGACCCCAAGGC 900
DB 1455 GGAATCCTCCCGTATGGTCTCAGCTGATCGAAGAGCATAGCCTTCAAGACCTCAAGGC 1514
QY 901 GAGCCCTCAGCGAAGCGGCTCGACAGTGTGAGCTTCCGCGACACTACTGTGAGAAGGACCT 960
DB 1515 GAGCCCTCAGCGAAGCGGCTCGACAGTGTGAGCTTCCGCGACACTACTGTGAGAAGGAACT 1574
QY 961 AAACCTTGCCTGCTCTCAGCGTGGCAAAACAGATACACGCGCTCTGCTCGGTGTGGA 1020
DB 1575 AAACCTTGCCTGCTCTCAGCGTGGCAAAACAGATACACGCGCTCTGCTCGGTGTGGA 1634
QY 1021 AGCCACAGAGATCAGCATGCTTTTCTCACCGACTACATCAAGAGTGCACCGGTCTCAG 1080
DB 1635 AGCCACAGAGATCAGCATGCTTTTCTCACCGACTACATCAAGAGTGCACCGGTCTCAG 1694
QY 1081 TAAATATTGCTCGGACAAAGAGCGGCGGAGTATATGATGATGCAAAACAGGTGCGTG 1140
DB 1695 TAAATATTGCTCGGACAAAGAGCGGCGGAGTATATGATGATGCAAAACAGGTGCGTG 1744
QY 1141 CGGTGCTCTCTCAGCTAGGGGACTCGTTTCTTAGTGGTCAATTCAGGATGATGAGTTCGATT 1200
DB 1745 -----CAGGTATGAGTTCGATT 1761
QY 1201 TGCCATGCCATGTCAAAGAACTTGTTCAGGCTCAGTGCACCTCAACACCCCGTCTCCT 1260
DB 1762 TGCCATGCCATGTCAAAGAACTTGTTCAGGCTCAGTGCACCTCAACACCCCGTCTCCT 1821
QY 1261 GGAATTTGACACTCGCGCTCGGCTGTATAGTACGATCGGCTCGGCGCGCTGTTCGA 1320
DB 1822 GAAATTTGACACTCGCGCTCGGCTGTATAGTACGATCGGCTCGGCGCGCTGTTCGA 1881
QY 1321 AGCAAAAGCTGGTGGTTTTCGTTACCGACACATTTGTATCCACCTTGACATTTTCAACA 1380
DB 1882 AGCAAAAGCTGGTGGTTTTCGTTACCGACACCTTTGTATCCACCTTGACATTTTCAACA 1941
QY 1381 CTTCTTCCCGCGAGAAAGCAAGCATTTGGCGGAAATCTATCTCGGCTTACATAGCAG 1440
DB 1942 CTTCTTCCCGCGAGAAAGCAAGCATTTGGCGGAAATTTCTATCTCGGCTTACATAGCAG 2001
QY 1441 ATAGTCTTCTGATGGACAAACCGCTGCTGGCGCAACAAAGGCTTCTCGGCGCTCTCCAA 1500
DB 2002 ATAGTCTTCTGATGGACAAACCGCTGCTGGCGCAACAAAGGCTTCTCGGCGCTCTCCAA 2061
QY 1501 TCAGCTGTGACCCCATCTCATTTGCCAGATACAGCATCGAAGTCTGATCGGCAATGG 1560
DB 2062 TCAGCTGTGACCCCATCTCATTTGCCAGATACAGCATCGAAGTCTGATCGGCAATGG 2121
QY 1561 TCATTTACCTGTTTCATGGTTCGGAGACCCGGGACAGTGGTCCCAACAGTCCCAAGCAG 1620
DB 2122 TCATTTACCTGTTTCATGGTTCGGAGACCCGGGACAGTGGTCCCAACAGTCCCAAGCAG 2181
QY 1621 GTACGACAAAAGTCTGCTGGGACCAACTCCGCGCAAGCTACGAGAACCCCGGGGCCAA 1680
DB 2182 GTACGACAAAAGTCTGCTGGGACCAACTCCGCGCAAGCTACGAGAACCCCGGGGCCAA 2241
QY 1681 GTCCAGAGCGGCCCAACGCTGCTCGAAATCGAGTGTGCAAGCAGCAGTATTTTCAAGGA 1740
DB 2242 GTCCAGAGCGGCCCAACGCTGCTCGAAATCGAGTGTGCAAGCAGCAGTATTTTCAAGGA 2301
QY 1741 GCTCCGAGCGCGCTATGGCTGAGCATCTCATCAGCTGGGTTTCGGCTCAGAACG 1800
DB 2302 GCTCCGAGCGCGCTATGGCTGAGCATCTCATCAGCTGGGTTTCGGCTCAGAACG 2361
QY 1801 CCGTTCAAGTGTGTTTCAATTTGGAACGAGACGCTCTTAGTTTGGAAAGGATATG 1860
DB 2362 CCGTTCAAGTGTGTTTCAATTTGGAACGAGACGCTCTTAGTTTGGAAAGGATATG 2421
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QY 1861 GAAGGGCCATACGATCGGTCAACGAGGTGCTGCAGAGTTGTGGCTAGCCTGGTGCCA 1920
|||||
Db 2422 GAAGGGCCATACGATCGGTCAACGAGGTGCTGCAGAGTTGTGGCTAGCCTGGTGCCA 2481

QY 1921 GCAGCATAG 1929
|||||
Db 2482 GCAGCATAG 2490

RESULT 10

US-09-352-168-32

; Sequence 32, Application US/09352168A

; Patent No. 6211435

; GENERAL INFORMATION:

; APPLICANT: Crasta, Oswald R.

; APPLICANT: Duvick, Jonathan P.

; APPLICANT: Folkerts, Otto

; APPLICANT: Gilliam, Jacob T.

; APPLICANT: Maddox, Joyce R.

; TITLE OF INVENTION: Amino Polyol Amine Oxidase

; TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use

; FILE REFERENCE: 0875

; CURRENT APPLICATION NUMBER: US/09/352.168A

; CURRENT FILING DATE: 1999-07-12

; EARLIER APPLICATION NUMBER: 60/092,936

; EARLIER FILING DATE: 1998-07-25

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 32

; LENGTH: 2490

; TYPE: DNA

; ORGANISM: Unknown

; FEATURE:

; OTHER INFORMATION: GST-glyc(-)APAO open reading frame, 2490 nt; GST

; OTHER INFORMATION: and linker, nt 1-687; Glyc (-) APAO, nt 688-2490;

; OTHER INFORMATION: mutation in putative glycosylation sites in bold

; OTHER INFORMATION: and underlined, nt 1288-1290 (AAT-> TCC) and nt

; OTHER INFORMATION: 1303-1305 (AGC-> AAC).

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (1)...(2487)

; NAME/KEY: misc_feature

; LOCATION: (1)...(687)

; OTHER INFORMATION: GST and linker

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (688)...(2490)

; OTHER INFORMATION: Glyc (-) APAO

; FEATURE:

; NAME/KEY: mutation

; LOCATION: (1288)...(1290)

; OTHER INFORMATION: mutation in putative glycosylation site (AAT->TCC)

; FEATURE:

; NAME/KEY: mutation

; LOCATION: (1303)...(1305)

; OTHER INFORMATION: mutation in putative glycosylation site (AGC->AAC)

; US-09-352-168-32

Query Match

Best Local Similarity 82.7%; Score 1596.2; DB 4; Length 2490;

Matches 1765; Conservative 0; Mismatches 38; Indels 126; Gaps 2;

QY 1 ATGGCAGTTCACCGAGCTACATCAATCCCCCAACCTCGCTCCCGCAGGAGTTTCC 60

Db 688 ATGGCAGTTCACCGAGCTACATCAATCCCCCAACCTCGCTCCCGCAGGAGTTTCT 747

QY 61 CACATCGCGTAGGCCCAAGCGAGGTATGTGACAATAGCTGGACAGATTGGACAA 120

Db 748 CACGTCGCGTAGGCCCAAGCGAGGTATGTGACAATAGCTGGACAGATTGGACAA 807

QY 121 GACGCTTTGGCGTGACAGCCAGCCCTACGAGAACAGGTGCCCAAGCATTCGCCAAT 180

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Db 808 GACGCTTGGGCGTGACAGACCCCTGCTACGAGAAACAGGTTGCCCAAGCATTCGCCAAT 867
QY 181 CTGGAGCTTGCCTTGTGTCAGTTGGAGCCTCTTCAAAACAGCTCACCAGGTCAATTAC 240
Db 868 CTGGAGCTTGCCTTGTGTCAGTTGGAGCCTCTTCAAAACAGCTCACCAGGTCAATTAC 927
QY 241 TACATCGTGCAGTACGCCCGCAGCAAACTCACCGCAATTGGAGATGGGTGAAGTCTACC 300
Db 928 TACATCGTGCAGTACGCCCGCAGCAAACTCACCGCAATTGGAGATGGGTGAAGTCTACC 987
QY 301 TTTGCCCTTGACAGGCTCCCTCTTGACACGCTGGTGCACGCTTACCGGCTTGGCTTCAACT 360
Db 988 TTTGCCCTTGACAGGCTCCCTCTTGACACGCTGGTGCACGCTTACCGGCTTGGCTTCAACT 1047
QY 361 GAATACCTCTTTGAGTTGATGCCACGGCCTGGTGCCAGGACACTCGACCCCAAGACAAAC 420
Db 1048 GAATACCTCTTTGAGTTGATGCCACGGCCTGGTGCCAGGACACTCGACCCCAAGACAAAC 1107
QY 421 GTTGGGACGTGTAGTGGTGGGCGCTTGAGCGGTTTGAGAGCGGCACGACCCCAAGTC 480
Db 1108 GTTGGGACGTGTAGTGGTGGGCGCTTGAGCGGTTTGAGAGCGGCACGACCCCAAGTC 1167
QY 481 CAGGCCCGCGTCTGCTGCTGCTGCTTCTTGGAGCGATGGATCGTAGGGGSAAGACT 540
Db 1168 CAGGCCCGCGTCTGCTGCTGCTGCTTCTTGGAGCGATGGATCGTAGGGGSAAGACT 1227
QY 541 CTGAGCGTACAAATCGGTCCCGGCGAGGACACTATCAACGACCTCGGCGCTGGTGGATC 600
Db 1228 CTGAGCGTACAAATCGGTCCCGGCGAGGACACTATCAACGACCTCGGCGCTGGTGGATC 1287
QY 601 AATGACAGCAACCAAGCAAGTATCCAGATTGTTTGAAGAATTTTCATTTGGAGGCGGAG 660
Db 1288 TCCGACAGCAACCAAGCAAGTATCCAGATTGTTTGAAGAATTTTCATTTGGAGGCGGAG 1347
QY 661 CTCAGAGGAGCGACCGGAATTCATCCATCAAGCACAAGACGGTACACCACACTACAGCT 720
Db 1348 CTCAGAGGAGCGACTGGAAATTCATCCATCAAGCACAAGACGGTACACCACACTACAGCT 1407
QY 721 CTTTATGTGACTCCCGGTTAAGCACAAATCCCACTTTGTGATGAGACCTCTGTGCGAGTGT 780
Db 1408 CTTTATGTGACTC----- 1421
QY 781 AGAATACAGTCACTGACTCCACTTCGCTCAGCTGAGCGGAGGAGTTGCAAGTGCACCTTCG 840
Db 1422 -----CTTGTCTGAGCGAGGAGTTGCAAGTGCACCTTCG 1454
QY 841 GGAATCCTCCCGTATGTTCTCAGCTGATCGAAGAGTATAGCTTTGAAGACCCCAAGGC 900
Db 1455 GGAATCCTCCCGTATGTTCTCAGCTGATCGAAGAGTATAGCTTTGAAGACCCCAAGGC 1514
QY 901 GAGCCCTCAGCGAAGCGGCTCGACAGTGTGAGCTTGGCGCACTACTGTGAGAGGACCT 960
Db 1515 GAGCCCTCAGCGAAGCGGCTCGACAGTGTGAGCTTGGCGCACTACTGTGAGAGGAACT 1574
QY 961 AAACCTGCTGCTCTCTCAGCGTGGCAACACAGATCACACGCGCTCTGCTGGTGTGA 1020
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QY 1021 AGCCACAGAGTACAGTATGCTTTTCTACCGACTACATCAAGAGTGCCACCGGTTCTCAG 1080
Db 1635 AGCCACAGAGTACAGTATGCTTTTCTACCGACTACATCAAGAGTGCCACCGGTTCTCAG 1694
QY 1081 TAATATTTCTCGACAAAGAACGCGGCGAGTATATCGATGCAAAACAGTCCGCTG 1140
Db 1695 TAATATTTCTCGACAAAGAACGCGGCGAGTATATCGATGCAAAACAGTCCGCTG 1744
QY 1141 CGGTGCTCTCAGGTAGGGGACTCGCTTTCTTAGTGGTCAATTCAGGTATGCAAGTCCGATT 1200
Db 1745 -----CAGGTATGCAAGTCCGATT 1761
QY 1201 TGCCATGCCATGTCAAAGGAACTGTTCCAGGCTCAGTGCACCTCAACACCCCGCTCGCT 1260
Db 1762 TGCCATGCCATGTCAAAGGAACTGTTCCAGGCTCAGTGCACCTCAACACCCCGCTCGCT 1821

QY 1261 GGAATTGAGCAGTCGGGCTCGCTGTATAGTACGATCGSCCTCGSGCGCGTGTCCGA 1320
Db 1822 GAAATTGAGCAGTCGGGATCCGGCTGTACAGTACGATCGGCCCTCGGGCGCGTGTCCGA 1881
QY 1321 AGCAAAAGGTGGTGGTTTCGTTACCGACAACATTTGTATCCCACTTGACATTTTCACCA 1380
Db 1882 AGCAAAAGGTGGTGGTTTCGTTACCGACAACCTTGTATCCCACTTGACATTTTCACCA 1941
QY 1381 CCTCTTCCCGCGAGAGCAAGCATTTGGCGGAAAAATCTATCTCCGCTACTATACCAAG 1440
Db 1942 CCTCTTCCCGCGAGAGCAAGCATTTGGCGGAAAAATCTATCTCCGCTACTATACCAAG 2001
QY 1441 ATAGCTCTTCGTATGGGACAACCGTGTGTGGCGGACAAGGCTTCTCGGGCGTCTCCAA 1500
Db 2002 ATAGCTCTTCGTATGGGACAAGCGTGTGTGGCGGACAAGGCTTCTCGGGCGTCTCCAA 2061
QY 1501 TCGAGCTGTGACCCCATCTCATTTTGCAGAGATACCAAGCATCGAAATCGATCGGCAATGG 1560
Db 2062 TCGAGCTGTGACCCCATCTCATTTTGCAGAGATACCAAGCATCGAGCTCGATCGACAATGG 2121
QY 1561 TCCATTACCTGTTTCATGTCGGAGACCCGGAGGGAAGTGGTCCCAACAGTCCAAAGCAG 1620
Db 2122 TCCATTACCTGTTTCATGTCGGAGACCCGGAGGGAAGTGGTCCCAACAGTCCAAAGCAG 2181
QY 1621 GTACGACAAAAGTCTGTCTGGGACCAACTCGCGCGACGCTACGAGAACGCGGGGCGCCAA 1680
Db 2182 GTACGACAAAAGTCTGTCTGGGACCAACTCGCGCGACGCTACGAGAACGCGGGGCGCCAA 2241
QY 1681 GTCCAGAGCGCGCAACGTGCTCGAATCGAGTGTGTCGAAGCAGCAGTATTTCCAAAGGA 1740
Db 2242 GTCCAGAGCGCGCAACGTGCTCGAATCGAGTGTGTCGAAGCAGCAGTATTTCCAAAGGA 2301
QY 1741 GCTCGAGCGCGCTATGGGCTGAACGATCTCATCACACTGGTTCGGGCGTCCAGAACG 1800
Db 2302 GCTCGAGCGCGCTATGGGCTGAACGATCTCATCACACTGGTTCGGGCGTCCAGAACG 2361
QY 1801 CCGTTCAAGTGTGTTTCAATTCGTTGGAACGAGACGCTCTTAGTTTGGAAAGGCTATATG 1860
Db 2362 CCGTTCAAGAGTGTTCATTCGTTGGAACGAGACGCTCTTAGTTTGGAAAGGCTATATG 2421
QY 1861 GAAGGGGCCATACGATCGGGTCAACAGAGTGCTGCAGAAAGTGTGGCTAGCCTGGTGCCA 1920
Db 2422 GAAGGGGCCATACGATCGGGTCAACAGAGTGCTGCAGAAAGTGTGGCTAGCCTGGTGCCA 2481
QY 1921 GCACATAG 1929
Db 2482 GCACATAG 2490

RESULT 11

US-09-352-159-7
; Sequence 7, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
; APPLICANT: DuVick, Jonathan P.
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; FILE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
; FILE REFERENCE: 1134
; CURRENT APPLICATION NUMBER: US/09/352,159A
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: 60/092,936
; EARLIER FILING DATE: 1998-07-25
; EARLIER APPLICATION NUMBER: 60/135,391
; EARLIER FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 1442
; TYPE: DNA
; ORGANISM: Exophiala spinifera

; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(646)
; NAME/KEY: Intron
; LOCATION: (647)...(699)
; NAME/KEY: CDS
; LOCATION: (700)...(1439)
US-09-352-159-7

Query Match 68.4%; Score 1319; DB 4; Length 1442;
Best Local Similarity 93.5%; Pred. No. 0;
Matches 1417; Conservative 0; Mismatches 25; Indels 73; Gaps 1;

QY 415 GACAAAGTTGCGGACGTGGTAGTGGTGGCGCTGGCTTTGAGCGGTTTGAGACGSCACGC 474
Db 1 GACACGTTGCGGACGTGGTAGTGGTGGCGCTGGCTTTGAGCGGTTTGAGACGSCACGC 60
QY 475 AAAGTCCAGGCGCGCGTCTGTCTGCTCGCTTCTTGAAGCGATGGATCGTGTAGGGGGA 534
Db 61 AAAGTCCAGGCGCGCGTCTGTCTGCTCGCTTCTTGAAGCGATGGATCGTGTAGGGGGA 120
QY 535 AAGACTCTGAGCGTACAATCGGGTCCCGGACGAGCACTATCAACGACCTCGGCGCTCGG 594
Db 121 AAGACTCTGAGCGTACAATCGGGTCCCGGACGAGCACTATCAACGACCTCGGCGCTCGG 180
QY 595 TGGATCAATGACAGCAACCAACGAAAGTATCCAGATTGTTTGAAGATTTCATTTGGAG 654
Db 181 TGGATCAATGACAGCAACCAACGAAAGTATCCAGATTGTTTGAAGATTTCATTTGGAG 240
QY 655 GCGGAGCTCCAGAGACGACCGGAAATTCATTCATCAAGCAACAGAGCGGTACACCACT 714
Db 241 GCGGAGCTCCAGAGACGACCTGGAAATTCATTCATCAAGCAACAGAGCGGTACACCACT 300
QY 715 ACAGCTCCCTATATGGTGACCTCCCGGTAAAGCAACATCCCACTTTGTGATGAGACCTCTGTC 774
Db 301 ACAGCTCCCTATATGGTGACCTC----- 320
QY 775 GAGTGTAGAATACAGTACTGACTCCACTTCGTTCAGCTGAGCGAGGAGTTGCAAGTGC 834
Db 321 -----CTTGCTGAGCGAGGAGTTGCAAGTGC 347
QY 835 ACTTGGGAACTCCTCCCGTATGGTCTCAGCTGATCGAAGAGTATAGCCTTGAAGACCC 894
Db 348 ACTTGGGAACTCCTCCCGTATGGTCTCAGCTGATCGAAGAGCATAGCCTTCAAGACCT 407
QY 895 CAAGCGAGCCCTCAGGCGAAGCGCTGCACAGTGTGAGCTTCGGGCACTACTGTGAGAA 954
Db 408 CAAGCGAGCCCTCAGGCGAAGCGGCTGCACAGTGTGAGCTTCGGGCACTACTGTGAGAA 467
QY 955 GGACCTAAACTTGCCTGCTTCTCAGCGTGGCAACACAGATCACAGCGCTCTGCTCGG 1014
Db 468 GGAACCTAAACTTGCCTGCTTCTCAGCGGTAGCAAAACAGATCACAGCGCTCTGCTCGG 527
QY 1015 TGTGGAAGCCACGAGTACGATGCTTTTCTCAGCGTACATCAAGAGTGCACCGG 1074
Db 528 TGTGGAAGCCACGAGTACGATGCTTTTCTCAGCGTACATCAAGAGTGCACCGG 587
QY 1075 TCTCAGTAAATATTGCTCGGACAAGAAAGACGCGGCGCACTATATCGGATGCAAAACAG 1134
Db 588 TCTCAGTAAATATTCTCGGACAAGAAAGACGCGGCGAGTATGTCCGATGCAAAACAG 647
QY 1135 TGGTGGGTGCTCCTCTCAGGTAGGGGACTGCTTTCTTAGTGTGCTATTCAGGTATGCAG 1194
Db 648 TGGTGTGTGTGCTCTCAGGTGGGAGTCTGTTTCTCAGTGTGCTATTCAGGTATGCAG 707
QY 1195 TCGATTTGCCATGCCATGTCAAGGAACTTGTTCAGGCTCAGTGCACCTCAACACCCGC 1254
Db 708 TCGATTTGCCATGCCATGTCAAGGAACTTGTTCAGGCTCAGTGCACCTCAACACCCGC 767
QY 1255 GTGCTGGAATTGAGCAGTCGGGCTCGGCTGTATAGTACGATCGGCGCGCGGTG 1314
Db 768 GTCGCTGAATTGAGCAGTCGGCATCCGGCTGTACAGTACGATCGGCTCGGCGCGGTG 827

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QY 1315 TTCGAAGCAAAAAGGTGGTTCGTTTCGTTACCGACACATGTTATCCACCCTTGACATTT 1374
Db 828 TTCGAAGCAAAAAGGTGGTTCGTTTCGTTACCGACACCTTGTATCCACCCTTGACATTT 887
QY 1375 TCACCACCTCTTCCTCCGCGGAGAACAGCATTTGGCGGAAAAATCTATCCTCGGCTACTAT 1434
Db 888 TCACCACCTCTTCCTCCGCGGAGAACAGCATTTGGCGGAAAAATCTATCCTCGGCTACTAT 947
QY 1435 AGCAAGATAGTCTTCGTATGGGACAAACCGTGGTGGCGGAAACAAGGCTTCTCGGGCGTC 1494
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QY 1495 CTCCAATCGAGCTGTGACCCCATCTCATTTGCCAGAGATACCAAGCTCGATCGG 1554
Db 1008 CTCCAATCGAGCTGTGACCCCATCTCATTTGCCAGAGATACCAAGCTCGATCGA 1067
QY 1555 CAATGGTCCATTACCTGTTTCATGGTCGGAGACCCGGGACGGAAGTGGTCCCAACAGTCC 1614
Db 1068 CAATGGTCCATTACCTGTTTCATGGTCGGAGACCCGGGACGGAAGTGGTCCCAACAGTCC 1127
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Db 1128 AAGCAGGTACGACAAAAGTCTGTCTGGGACCAACTCTCGGCGACGCTACGAGAACGCCGGG 1187
QY 1675 GCCCAAGTCCAGAGCGCGCAACGTCTCGAAATCGAGTGGTTCGAGCAGCATTTTC 1734
Db 1188 GCCCAAGTCCAGAGCGCGCAACGTCTCGAAATCGAGTGGTTCGAGCAGCATTTTC 1247
QY 1735 CAAGAGCTCCGAGCGCGCTCTATGGGCTGAACGATCTCATCACACTGGTTCGGCGCTC 1794
Db 1248 CAAGAGCTCCGAGCGCGCTCTATGGGCTGAACGATCTCATCACACTGGTTCGGCGCTC 1307
QY 1795 AGAAGCGCTTCAAGTGTGTTCATTTGTTGGAACGAGACGCTTTAGTTTGGAAAGG 1854
Db 1308 AGAAGCGCTTCAAGTGTGTTCATTTGTTGGAACGAGACGCTTTAGTTTGGAAAGG 1367
QY 1855 TATATGAAGGGGCCATACATCGGTCACAGAGTGCTGCAGAGTGTGCTGACAGATTTGTGCTAGCCGTG 1914
Db 1368 TATATGAAGGGGCCATACATCGGTCACAGAGTGCTGCAGAGTGTGCTGACAGATTTGTGCTAGCCGTG 1427
QY 1915 GTGCCAGCAGCATAG 1929
Db 1428 GTGCCAGCAGCATAG 1442

RESULT 12
; Sequence 7, Application US/09352168A
; Patent No. 6211435
; GENERAL INFORMATION:
; APPLICANT: Crasta, Oswald R.
; APPLICANT: Duwick, Jonathan P.
; APPLICANT: Folkerts, Otto
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; FILE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
; FILE REFERENCE: 0875
; CURRENT APPLICATION NUMBER: US/09/352,168A
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: 60/092,936
; EARLIER FILING DATE: 1998-07-25
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 1442
; TYPE: DNA
; ORGANISM: Exophiala spinifera
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(646)
; NAME/KEY: Intron
; LOCATION: (647)...(699)
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; NAME/KEY: CDS
; LOCATION: (700)...(1439)
US-09-352-168-7

Query Match      68.4%; Score 1319; DB 4; Length 1442;
Best Local Similarity 93.5%; Pred. No. 0;
Matches 1417; Conservative 0; Mismatches 25; Indels 73; Gaps 1;

QY 415 GACAAAGTTGCGGAGCTGGTAGTGGTGGCGCTGGCTTGGAGCGGTTTGGAGACGCGCAGC 474
Db 1 GACAAAGTTGCGGAGCTGGTAGTGGTGGCGCTGGCTTGGAGCGGTTTGGAGACGCGCAGC 60
QY 475 AAAGTCCAGGCGCGGCTGTCTCTCGCTTCGTTCTTGGAGGCGATCGATCGTGTAGGGGGA 534
Db 61 AAAGTCCAGGCGCGGCTGTCTCTCGCTTCGCTTCGTTCTTGGAGCGATGATCGTGTAGGGGGA 120
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Db 121 AAGACTCTGAGCGGTACAATCGGCTCCGCGAGGAGCAGTATCAAGAGCTCTCGGCGCTGCG 180
QY 595 TGGATCAATGACAGCAACCAAGCGAAGTATCCAGATTGTTTGAAGATTTCATTTGGAG 654
Db 181 TGGATCAATGACAGCAACCAAGCGAAGTATCCAGATTGTTTGAAGATTTCATTTGGAG 240
QY 655 GCGAGCTCCAGAGGACGACCGGAAATTCATTCATCAAGCACAGAGCGTACAAACCACT 714
Db 241 GCGAGCTCCAGAGGACGACCTGGAAATTCATTCATCAAGCACAGAGCGTACAAACCACT 300
QY 715 ACAGCTCTCTTATGGTGACTCCCGGTAGAGCAATCCACACTTTGTGATGAGACCTCTGTC 774
Db 301 ACAGCTCTCTTATGGTGACTC----- 320
QY 775 GAGTGTAGAATACATCACTCACTTCCACTTCCGTCGAGCTGAGCGAGGAGTTGCAAGTGC 834
Db 321 -----CTGCTGAGCGAGGAGTTGCAAGTGC 347
QY 835 ACTTCGGAACCTCTCCCGCTATGCTCTACGCTGATGAGAGATATAGCCTTGAAGACCC 894
Db 348 ACTTCGGAACCTCTCCCGCTATGCTCTACGCTGATGAGAGCATAGCCTTCAAGACCT 407
QY 895 CAAGCGAGCCCTCAGGCGAAGCGCTCGACAGTGTAGCTTCGCGCAGTCTCGGCTACTGTGAGAA 954
Db 408 CAAGCGAGCCCTCAGGCGAAGCGCTCGACAGTGTAGCTTCGCGCAGTCTCGGCTACTGTGAGAA 467
QY 955 GGACCTAAACTTGCCTGCTGTTCTCAGCGTGGCAAAACAGATCACACGCGCTCTGCTCGG 1014
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Db 528 TGTGGAAGCCCAAGAGATCAGCATGCTTTTCTCACCGACTACATCAAGAGTGCACCCCG 587
QY 1075 TCTCAGTAATATTGCTCGGACAAAGAGACGGCGGCGAGTATGATGATGCAAAACAGG 1134
Db 588 TCTCAGTAATATTGCTCGGACAAAGAGACGGCGGCGAGTATGTCGATGCAAAACAGG 647
QY 1135 TCGCTGGGTGCTCTCTCAGTAGGGGACTCGTTTCTTAGTGGTTCATTCAGAGTATGCGAG 1194
Db 648 TCGCTGGGTGCTCTCTCAGTAGGGGACTCGTTTCTTAGTGGTTCATTCAGAGTATGCGAG 707
QY 1195 TCGATTGTCATGCCATGTCAAAGGAACTTTTCCAGGCTCAGTGCACCTCAACACCCCG 1254
Db 708 TCGATTGTCATGCCATGTCAAAGGAACTTTTCCAGGCTCAGTGCACCTCAACACCCCG 767
QY 1255 GTCGCTGGAATTGAGCAGTCCGGCTCGCGCTGTATAGTACGATCGGCGCTCGGCGCGCTG 1314
Db 768 GTCGCTGAAATTGAGCAGTCCGGCTGTACAGTAGATCGGCTCGGCGCTCGGCGCGCTG 827
QY 1315 TTCCGAAGCAAAAAGGTGGTTCGTTTCGTTACCGACACATTTGTATCCACCCTTGACATTT 1374
Db 828 TTCCGAAGCAAAAAGGTGGTTCGTTTCGTTACCGACACCTTGTATCCACCCTTGACATTT 887
QY 1375 TCACCACCTCTTCCTCCGCGGAGAACAGCATTTGGCGGAAAAATCTATCCTCGGCTACTAT 1434
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Db 888 TCACCACTCTTCCCGCCGAGAGCAAGCATTTGGCGGAAAATCTATCTCGGCTACTAT 947
QY 1435 AGCAAGATAGTCTTCGTATGGGACAAACCGTGTGGCGGCAAAAGAGTCTTCGGGCGTC 1494
Db 948 AGCAAGATAGTCTTCGTATGGGACAAACCGTGTGGCGGCAAAAGAGTCTTCGGGCGTC 1007
QY 1495 CTCGAATCGAGCTGTGACCCCATCTCATTTGCCAGAGATACCAGCATCAAAGTCGATCGG 1554
Db 1008 CTCGAATCGAGCTGTGACCCCATCTCATTTGCCAGAGATACCAGCATCAAAGTCGATCGA 1067
QY 1555 CAATGTTCCATTACCTGTTTCATGTGTCGGAGCCCGGAGCGGAAGTGTCCCAACAGTCC 1614
Db 1068 CAATGTTCCATTACCTGTTTCATGTGTCGGAGCCCGGAGCGGAAGTGTCCCAACAGTCC 1127
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QY 1675 GCCCAAGTCCAGAGCGGCGCAACGTGCTCGAATCGAGTGTGTCGAAGCAGCATTTTC 1734
Db 1188 GCCCAAGTCCAGAGCGGCGCAACGTGCTCGAATCGAGTGTGTCGAAGCAGCATTTTC 1247
QY 1735 CAAGGAGCTCCGAGCGCGCTATGGGCTGAACGATCTCATCACACTGGGTTTCGGCGCTC 1794
Db 1248 CAAGGAGCTCCGAGCGCGCTATGGGCTGAACGATCTCATCACACTGGGTTTCGGCGCTC 1307
QY 1795 AGAAGCGGTTCAAGTGTGTTTCATTTGTTGGAACGGAGACGCTTTAGTTGGAAAGGG 1854
Db 1308 AGAAGCGGTTCAAGTGTGTTTCATTTGTTGGAACGGAGACGCTTTAGTTGGAAAGGG 1367
QY 1855 TATATGAGGGGCCATACGATCGGTCACAGAGGTGCTCGAAGTGTGTCGCTAGCCTG 1914
Db 1368 TATATGAGGGGCCATACGATCGGTCACAGAGGTGCTCGAAGTGTGTCGCTAGCCTG 1427
QY 1915 GTGCCAGCAGCATAG 1929
Db 1428 GTGCCAGCAGCATAG 1442
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RESULT 13
US-09-352-159-26
; Sequence 26, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
; APPLICANT: Duwick, Jonathan P.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
; FILE REFERENCE: 1134
; CURRENT APPLICATION NUMBER: US/09/352,159A
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: 60/092,936
; EARLIER FILING DATE: 1998-07-25
; EARLIER APPLICATION NUMBER: 60/135,391
; EARLIER FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 2976
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Barley alpha amylase signal sequence: BEST1
; OTHER INFORMATION: mature: artificial spacer: and K:trAPAO. For
; OTHER INFORMATION: plant expression.
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (1)...(72)
; OTHER INFORMATION: Barley alpha amylase signal sequence
; FEATURE:
; NAME/KEY: mat_peptide
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; LOCATION: (73)...(1545)
; OTHER INFORMATION: BEST1 mature
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1546)...(1584)
; OTHER INFORMATION: spacer sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1585)...(2973)
; OTHER INFORMATION: K:trAPAO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2973)
; NAME/KEY: misc_feature
; LOCATION: (1585)...(1587)
; OTHER INFORMATION: Extra lysine
US-09-352-159-26

Query Match 62.8%; Score 1212.2; DB 4; Length 2976;
Best Local Similarity 90.2%; Pred. No. 0;
Matches 1372; Conservative 0; Mismatches 23; Indels 126; Gaps 2;

QY 409 ACCCCAGACAAGCTTCCGGAGCTGTGTAGTGTGGCGCTGCTGAGCGGTTTGGAGACG 468
Db 1582 AGCAAGAGCAACGTTTCGGAGCTGTGTAGTGTGGCGCTGCTGAGCGGTTTGGAGACG 1641
QY 469 GCACGCAAGTCCAGCGCGGCTCTGCTCCCTCGCTTCTTGAGCGCATGATCGTGTA 528
Db 1642 GCACGCAAGTCCAGCGCGGCTCTGCTCCCTCGCTTCTTGAGCGCATGATCGTGTA 1701
QY 529 GGGGGAAGACTCTTGAGCGTACAATCGGTCCTCCGCGAGGAGCTATCAAGCACTCCGC 588
Db 1702 GGGGGAAGACTCTTGAGCGTACAATCGGTCCTCCGCGAGGAGCTATCAAGCACTCCGC 1761
QY 589 GCTGCGTGGATCAATGACAGCAACCAAGGATATCCAGATCTGTTTGAAGATTTTCAT 648
Db 1762 GCTGCGTGGATCAATGACAGCAACCAAGGATATCCAGATCTGTTTGAAGATTTTCAT 1821
QY 649 TTGGAGGGCGAGCTCCAGAGGAGCGCGGAAATTCATCCATCAAGCAACAGCGGTACA 708
Db 1822 TTGGAGGGCGAGCTCCAGAGGAGCGCTGGAATTCATCCATCAAGCAACAGCGGTACA 1881
QY 709 ACCACTACAGCTCCTTATGTTGACTCCCGGCTAAGCAACATCCCACTTTGTGATGAGCC 768
Db 1882 ACCACTACAGCTCCTTATGTTGACTC----- 1907
QY 769 TCTGTCGAGTGTAGATACAGTCACTGACTCCACTTCGTCAGCTGAGCGAGGAGGTTGC 828
Db 1908 -----CTTGCTGAGCGAGGAGGTTGC 1928
QY 829 AAGTGCACCTTGGGAACTCCTCCCGTATGGTCTCAGCTGATCGAAGATATAGCCTTGA 888
Db 1929 AAGTGCACCTTGGGAACTCCTCCCGTATGGTCTCAGCTGATCGAAGATATAGCCTTGA 1988
QY 889 AGACCCCAAGGCGAGCCCTCAGCGGAAGCGGCTCGACAGTGTGAGCTTCGCGCACTACTG 948
Db 1989 AGACCTCAAGGCGAGCCCTCAGCGGAAGCGGCTCGACAGTGTGAGCTTCGCGCACTACTG 2048
QY 949 TGAGAAGGACCTAAACTTGCTGCTCTCAGCGTGGCAACCAAGATCAGACGCGCTCT 1008
Db 2049 TGAGAAGGACCTAAACTTGCTGCTCTCAGCGTGGCAACCAAGATCAGACGCGCTCT 2108
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Db 2109 GCTCGGTGTGGAAGCCACAGATCAGCATGCTTTTCTCAGCGACTACATCAAGATGC 2168
QY 1069 CACCGGTCTCAGTAATATTCTCGGACAAAGAGCGGCGGCGAGTATATCGGATGCAA 1128
Db 2169 CACCGGTCTCAGTAATATTCTCGGACAAAGAGCGGCGGCGAGTATATCGGATGCAA 2228
QY 1129 AACAGGTGCGTGGGTCCTCTCAGGTAGGGGACTCGTTCTTAGTGGTTCATTCAGGT 1188
Db 2229 AA-----CAGGT 2235
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| QY | 1189 | ATGCAGTCGATTTGCCATGCCATGTCAAAGAACTGTTCAGGCTCAGTGCACCTCAAC | 1248 |
| Db | 2236 | ATGCAGTCGATTTGCCATGCCATGTCAAAGAACTTGTTCAGGCTCAGTGCACCTCAAC | 2295 |
| QY | 1249 | ACCCCCGTCGCTGGAAATTGAGCAGTCGGCGTCCGGGTGTATAGTACGATCGGCCTCGGGC | 1308 |
| Db | 2296 | ACCCCCGTCGCTGAAATTGAGCAGTCGGCATCCGGCTGTACAGTACGATCGGCCTCGGGC | 2355 |
| QY | 1309 | GCCGTGTTCCGAAGCAAAAAGTGTGGTTTCGTTACCGACAACATGTATCCCAACCTTG | 1368 |
| Db | 2356 | GCCGTGTTCCGAAGCAAAAAGTGTGGTTTCGTTACCGACAACCTGTATCCCAACCTTG | 2415 |
| QY | 1369 | ACATTTTACCACCTCTTCCCGCGAGAAGCAAGCATTTGGGGAAAAATCTATCCTCGGC | 1428 |
| Db | 2416 | ACATTTTACCACCTCTTCCCGCGAGAAGCAAGCATTTGGGGAAAAATCTATCCTCGGC | 2475 |
| QY | 1429 | TACTATAGCAAGATAGTCTTCTGTATGGGACAACCCGTTGGCGCGACAAGGCTTCTCG | 1488 |
| Db | 2476 | TACTATAGCAAGATAGTCTTCTGTATGGGACAAGCCGTTGGCGCGACAAGGCTTCTCG | 2535 |
| QY | 1489 | GGCGTCTCCTCAATCGAGCTGTGACCCCATCTCATTTGCCAGAGATACCAGCATCGAAGTC | 1548 |
| Db | 2536 | GGCGTCTCCTCAATCGAGCTGTGACCCCATCTCATTTGCCAGAGATACCAGCATCGAAGTC | 2595 |
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| Db | 2596 | GATCGGCAATGTPCCATTACCTGTTTCATGTTCGGAGACCCGGGACCGAAAGTGTCCCAA | 2655 |
| QY | 1609 | CAGTCCAAGCAGGTAGCAGCAAAAAGTCTGTCTGGGACCAACTCCGCGAGCCTACGAGAAC | 1668 |
| Db | 2656 | CAGTCCAAGCAGGTAGCAGCAAAAAGTCTGTCTGGGACCAACTCCGCGAGCCTACGAGAAC | 2715 |
| QY | 1669 | GCCGGGGCCCCAAGTCCACAGCGCGCCCAACGTGCTCGAAATCGAGTGGTTCGAGCAGCAG | 1728 |
| Db | 2716 | GCCGGGGCCCCAAGTCCACAGCGCGCCCAACGTGCTCGAAATCGAGTGGTTCGAGCAGCAG | 2775 |
| QY | 1729 | TATTTCCAAAGGAGCTCCGAGCCGCTCTATGGGCTGAACGATCTCATCACACTGGGTTTCG | 1788 |
| Db | 2776 | TATTTCCAAAGGAGCTCCGAGCCGCTCTATGGGCTGAACGATCTCATCACACTGGGTTTCG | 2835 |
| QY | 1789 | GCCTCAGAACCCGTTCAAGTGTGTTTCATTTGTTGGAACGGAGAGCTTTAGTTTGG | 1848 |
| Db | 2836 | GCCTCAGAACCCGTTCAAGAGTGTTCATTTGTTGGAACGGAGAGCTTTAGTTTGG | 2895 |
| QY | 1849 | AAAGGATATATGGAAGGGGCCATAGATCGGGTCAACGAGTGCTCGAAGTTGTGGCT | 1908 |
| Db | 2896 | AAAGGATATATGGAAGGGGCCATACCATCGGGTCAACGAGTGCTCGAAGTTGTGGCT | 2955 |
| QY | 1909 | AGCCTGGTGCCAGCAGCATAG | 1929 |
| Db | 2956 | AGCCTGGTGCCAGCAGCATAG | 2976 |

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RESULT 14
US-09-352-168-26
; Sequence 26, Application US/09352168A
; Patent No. 6211435
; GENERAL INFORMATION:
; APPLICANT: Crasta, Oswald R.
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: Folkerts, Otto
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
; FILE REFERENCE: 0875
; CURRENT APPLICATION NUMBER: US/09/352,168A
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: 60/092,936
; EARLIER FILING DATE: 1998-07-25
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0

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; SEQ ID NO 26
; LENGTH: 2976
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Barley alpha amylase signal sequence: BEST1
; OTHER INFORMATION: mature: artificial spacer: and K:trAPAO. For
; OTHER INFORMATION: plant expression.
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (1)..(72)
; OTHER INFORMATION: Barley alpha amylase signal sequence.
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (73)..(1545)
; OTHER INFORMATION: BEST1 mature
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1546)..(1584)
; OTHER INFORMATION: Artificial spacer sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1585)..(2973)
; OTHER INFORMATION: K:trAPAO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2973)
; NAME/KEY: misc_feature
; LOCATION: (1585)..(1587)
; OTHER INFORMATION: Extra lysine
; US-09-352-168-26

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| Query Match | 62.8%; | Score 1212.2; | DB 4; | Length 2976; |
| Best Local Similarity | 90.2%; | Pred. No. 0; | | |
| Matches 1372; | Conservative 0; | Mismatches 23; | Indels 126; | Gaps |
| Qy | 409 | ACCCAGACACAGTTGGGACGTGGTAGTGGTGGCGCTGGCTTGAGCCGGTTTGAGACG | 468 | |
| Db | 1582 | AGCAAAAGACACAGTTGGGACGTGGTAGTGGTGGCGCTGGCTTGAGCCGGTTTGAGACG | 164 | |
| Qy | 469 | GCAGCAAAAGTCCAGGCGCGGCTGTCTCTGCTCGTCTTGGAGCGATGATCGTGTA | 528 | |
| Db | 1642 | GCAGCAAAAGTCCAGGCGCGGCTGTCTCTGCTCGTCTTGGAGCGATGATCGTGTA | 170 | |
| Qy | 529 | GGGGAAAGACTCTGACGTACAAATCGGGTCCGGCAGGACGACTATCAACGACCTCGGC | 588 | |
| Db | 1702 | GGGGAAAGACTCTGACGTACAAATCGGGTCCGGCAGGACGACTATCAACGACCTCGGC | 1761 | |
| Qy | 589 | GCTCGTGGATCAATGACACCAACCAAGCATCCAGATTCAGATCTGTTCAAGATTTTCAT | 648 | |
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| Qy | 709 | ACCACATACAGTCCCTTATGGTGACTCCCGGTAAGCANAATCCCACTTTGTGTAGAGACC | 768 | |
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| Qy | 769 | TCCTCGAGTGTAGAATACAGTCACTGACTCCACTTCGTCACGCTGACGAGGAGGTGCG | 828 | |
| Db | 1908 | -----CTTGCTGACGAGGAGGTGCG | 1928 | |
| Qy | 829 | AAGTGCACTTGGGAACCTCCTCCCGTATGGTCTCAGCTGATCGAAGAGTATAGCCTTGA | 888 | |
| Db | 1929 | AAGTGCACTTGGGAACCTCCTCCCGTATGGTCTCAGCTGATCGAAGAGTATAGCCTTGA | 1988 | |
| Qy | 889 | AGACCCCAAGGCGAGCCCTCAGGCAAGCGGCTCACAAGTGTAGCTTCGCGCACTACTG | 948 | |
| Db | 1989 | AGACCTCAAGGGAGCCCTCAGGCAAGCGGCTCACAAGTGTAGCTTCGCGCACTACTG | 2048 | |
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Qy 829 AAGTGCACCTTGGGAACCTCCCGCTATGCTCTCAGCTGATCGAAGAGTATAGCCCTTGA 888
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Qy 949 TGAGAAGGACCTTAAACTTGCCTGCTGTTCTCAGCGTGGCAAAACAGATCACACGCGCTCT 1008
Db 2076 TCAGAAGGAACCTAAACTTGCCTGCTGTTCTCGGCTAGCAAAACAGATCACACGCGCTCT 2135
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Db 2196 CACCGGTCTCAGTATATTTCTCGGACAGAAAGCGGGCAGTATATGCGATGCAA 2255
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Db 2983 AGCCTGTTGCCAGCAGCATAG 3003

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Job time : 96 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model
Run on: November 12, 2002, 03:21:40 ; Search time 140 Seconds
(without alignments)
4888.437 Million cell updates/sec

Title: US-09-771-045A-35
Perfect score: 1929
Sequence: 1 atggcaactgcacgcagctca.....gcttggtgccgcagcatag 1929

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 320260 seqs, 177392727 residues

Total number of hits satisfying chosen parameters: 640520

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA.*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
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- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | ID | Description |
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| 1 | 40.8 | 2.1 | 2491 | 10 | US-09-954-456-1583 |
| 2 | 40.8 | 2.1 | 2491 | 10 | US-09-880-107-2391 |
| 3 | 39 | 2.0 | 2389 | 10 | US-09-917-800A-1612 |
| 4 | 38 | 2.0 | 1386 | 10 | US-09-925-301-562 |
| 5 | 37.6 | 1.9 | 1095 | 10 | US-09-974-300-239 |
| 6 | 37.2 | 1.9 | 314 | 10 | US-09-960-352-3971 |
| 7 | 36.6 | 1.9 | 1575 | 10 | US-09-912-176-2 |
| 8 | 35.2 | 1.8 | 3276 | 10 | US-09-925-302-242 |
| 9 | 34.8 | 1.8 | 1949 | 10 | US-09-880-107-2398 |
| 10 | 34.8 | 1.8 | 3147 | 10 | US-09-925-300-617 |
| 11 | 34.8 | 1.8 | 4024 | 12 | US-10-044-090-86 |
| 12 | 34 | 1.8 | 2018 | 10 | US-09-925-301-376 |
| 13 | 34 | 1.8 | 2068 | 10 | US-09-880-107-1744 |
| 14 | 34 | 1.8 | 3370 | 12 | US-10-044-090-339 |
| 15 | 33.8 | 1.8 | 401 | 10 | US-09-795-668-1008 |
| 16 | 33.8 | 1.8 | 401 | 10 | US-09-795-668-1008 |
| 17 | 33.8 | 1.8 | 586 | 10 | US-09-349-015-3 |
| 18 | 33.8 | 1.8 | 1503841 | 10 | US-09-795-668-1 |
| 19 | 33.8 | 1.8 | 1503841 | 10 | US-09-795-668-1 |

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| 20 | 33.6 | 1.7 | 3708 | 10 | US-09-904-065-7 | Sequence 7, Appli |
| c 21 | 33.4 | 1.7 | 413 | 10 | US-09-728-446-947 | Sequence 947, App |
| c 22 | 33.2 | 1.7 | 351 | 10 | US-09-560-863-412 | Sequence 412, App |
| c 23 | 33 | 1.7 | 3033 | 9 | US-09-974-298-80 | Sequence 80, Appl |
| c 24 | 33 | 1.7 | 3056 | 10 | US-09-880-107-1765 | Sequence 1765, Ap |
| c 25 | 32.8 | 1.7 | 443 | 9 | US-10-046-935-1599 | Sequence 1599, Ap |
| c 26 | 32.8 | 1.7 | 465 | 10 | US-09-867-701-5341 | Sequence 5341, Ap |
| c 27 | 32.8 | 1.7 | 2163 | 10 | US-09-925-299-234 | Sequence 234, App |
| c 28 | 32.8 | 1.7 | 2609 | 10 | US-09-799-777-149 | Sequence 149, App |
| c 29 | 32.8 | 1.7 | 3141 | 10 | US-09-845-583-3 | Sequence 3, Appli |
| c 30 | 32.4 | 1.7 | 1319 | 10 | US-09-822-830A-383 | Sequence 383, App |
| c 31 | 32.2 | 1.7 | 1557 | 10 | US-09-962-290-7 | Sequence 7, Appli |
| c 32 | 32.2 | 1.7 | 13029 | 10 | US-09-815-242-4052 | Sequence 4052, Ap |
| c 33 | 32 | 1.7 | 981 | 10 | US-09-881-752A-283 | Sequence 283, App |
| c 34 | 32 | 1.7 | 1140 | 10 | US-09-861-289-15 | Sequence 15, Appl |
| c 35 | 32 | 1.7 | 3708 | 10 | US-09-904-065-5 | Sequence 5, Appli |
| c 36 | 32 | 1.7 | 3708 | 10 | US-09-904-065-9 | Sequence 9, Appli |
| c 37 | 32 | 1.7 | 13613 | 10 | US-09-861-289-3 | Sequence 3, Appli |
| c 38 | 31.8 | 1.6 | 979 | 10 | US-09-803-589-5 | Sequence 5, Appli |
| c 39 | 31.8 | 1.6 | 1428 | 10 | US-09-815-242-9802 | Sequence 9802, Ap |
| c 40 | 31.4 | 1.6 | 2623 | 10 | US-09-864-864-314 | Sequence 314, App |
| c 41 | 31 | 1.6 | 420 | 10 | US-09-864-761-10796 | Sequence 10796, A |
| c 42 | 31 | 1.6 | 645 | 10 | US-09-815-242-8018 | Sequence 8018, Ap |
| c 43 | 31 | 1.6 | 1202 | 10 | US-09-756-186-3 | Sequence 3, Appli |
| c 44 | 30.8 | 1.6 | 442 | 10 | US-09-764-878-392 | Sequence 392, App |
| c 45 | 30.8 | 1.6 | 579 | 10 | US-09-764-878-391 | Sequence 391, App |

ALIGNMENTS

RESULT 1
US-09-954-456-1583
; Sequence 1583, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C
; FILE REFERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954,456
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,638
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1583
; LENGTH: 2491
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-456-1583

Query Match 2.1%; Score 40.8; DB 10; Length 2491;
Best Local Similarity 58.1%; Pred. No. 0.01; Mismatches 0; Gaps 0;
Matches 72; Conservative 0; Indels 52

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| Qy | 417 | CAACGTTCCGACGTGTAGTGTGGCGCGTGGCTTGAGCGGTTTGGAGACGGCAGCGCAA | 476 |
| | | | |
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| Qy | 477 | AGTCACAGCGCGCGTGTGCTCTCGCTTTCTTGAGCGCGATGGATCGTTAGGGGGA | 536 |
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| Db | 143 | TCGCGATGACTCTGAGCTGAATGGTTGTTCTGGAAGCCCGGACCGTGTGGAGGCAG | 202 |
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| Qy | 537 | GACT 540 | |
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| Db | 203 | GACT 206 | |
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RESULT 2

US-09-880-107-2391

Sequence 2391, Application US/09880107

Patent No. US20020142981A1

GENERAL INFORMATION:

APPLICANT: Horne, Darci T.

APPLICANT: Vockley, Joseph G.

APPLICANT: Scherf, Uwe

APPLICANT: Gene Logic, Inc.

TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer

FILE REFERENCE: 44921-5028-WO

CURRENT APPLICATION NUMBER: US/09/880,107

PRIOR FILING DATE: 2001-06-14

PRIOR APPLICATION NUMBER: US 60/211,379

PRIOR FILING DATE: 2000-06-14

PRIOR APPLICATION NUMBER: US 60/237,054

PRIOR FILING DATE: 2000-10-02

NUMBER OF SEQ ID NOS: 3950

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2391

LENGTH: 2491

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: Genbank Accession No. US20020142981A1 M69177

US-09-880-107-2391

Query Match 2.1%; Score 40.8; DB 10; Length 2491;

Best Local Similarity 58.1%; Pred. No. 0.01;

Matches 72; Conservative 0; Mismatches 52; Indels 0; Gaps

NUMBER OF SEQ ID NOS: 896
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 242
LENGTH: 3276
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (125)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (455)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (1014)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (3276)
OTHER INFORMATION: n equals a,t,g, or c
US-09-925-302-242

Query Match 1.8%; Score 35.2; DB 10; Length 3276;
Best Local Similarity 52.8%; Pred. No. 0.81;
Matches 76; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 1613 GGTGTGAAGCCACGAGATCAGCATGCTTTCTCAGCGATACATCAAGAGTGCCACC 1072

DB 1366 GGGGAAGCTGCCTTATAATCTAAGTACTTTATCTACCTATTACAAAACAAGAAATC 1307

QY 1073 GGTCTCAGTAATATGTCGCGACAAGAAAGCGCGGAGTATATGCGATGCAAAACA 1132

DB 1306 TTTTCAGTAAATTTTTCAGAGCCCAAACTTTGTTTACACTATAGCTTAAGACAACA 1247

QY 1133 GGTGCGTGGGTGCTCTCAGGT 1156

DB 1246 GGTGTGGGTATGTTCACTGTGCT 1223

RESULT 9

US-09-880-107-2388

; Sequence 2388, Application US/09880107

; Patent No. US20020142981A1

; GENERAL INFORMATION:

; APPLICANT: Horne, Darci T.

; APPLICANT: Vockley, Joseph G.

; APPLICANT: Scherf, Uwe

; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer

; FILE REFERENCE: 44921-5028-WO

; CURRENT APPLICATION NUMBER: US/09/880,107

; CURRENT FILING DATE: 2001-06-14

; PRIOR APPLICATION NUMBER: US 60/211,379

; PRIOR FILING DATE: 2000-06-14

; PRIOR APPLICATION NUMBER: US 60/237,054

; PRIOR FILING DATE: 2000-10-02

; NUMBER OF SEQ ID NOS: 3950

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2388

; LENGTH: 1949

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: Genbank Accession No. US20020142981A1 M68840

US-09-880-107-2388

Query Match 1.8%; Score 34.8; DB 10; Length 1949;
Best Local Similarity 49.5%; Pred. No. 0.79;
Matches 90; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

QY 1215 AAAGGAACCTGTTCCAGCTCAGTGACCTCAACACCCCGCTGCTGGAATTTGAGCAGTC 1274

DB 763 AATGAGACCTCTCGGAGACCAAGTGAAGCTGAACCATCTGTCACTCAGCTTGACCAGTC 822

QY 1275 GGCGTCGGCTGTATAGTACGATCGGCTCGGGCGCGGTTCGGAAGCAAAAAGGTGCT 1334

DB 823 AAGTGACAACATCATCATAGAGAGCGCTGAACCATGAACATTATGATGCAAAATACGTAAT 882

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DB 883 TAATGCGATCCCTCCGACCTTGACTGCCAAGATTCACTTCAGACCAGAGCTTCCAGCAGA 942

QY 1395 GA 1396

DB 943 GA 944

RESULT 10

US-09-925-300-617

; Sequence 617, Application US/09925300

; Patent No. US20020151681A1

; GENERAL INFORMATION:

; APPLICANT: Steve Ruben,

; APPLICANT: Craig Rosen,

; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

; FILE REFERENCE: FA101

; CURRENT APPLICATION NUMBER: US/09/925,300

; CURRENT FILING DATE: 2001-08-10

; PRIOR APPLICATION NUMBER: PCT/US00/05988

; PRIOR FILING DATE: 2000-03-08

; PRIOR APPLICATION NUMBER: 60/124,270

; PRIOR FILING DATE: 1999-03-12

; NUMBER OF SEQ ID NOS: 1890

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 617

; LENGTH: 3147

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-925-300-617

Query Match 1.8%; Score 34.8; DB 10; Length 3147;
Best Local Similarity 49.5%; Pred. No. 1.1;
Matches 90; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

QY 1215 AAAGGAACCTGTTCCAGCTCAGTGACCTCAACACCCCGCTGCTGGAATTTGAGCAGTC 1274

DB 303 AATGAGACCTCTCTCGGAGACCAAGTGAAGCTGAACCATCTGTCACTCAGCTTGACCAGTC 362

QY 1275 GGCGTCGGCTGTATAGTACGATCGGCTCGGGCGCGGTTCGGAAGCAAAAAGGTGCT 1334

DB 363 AAGTGACAACATCATCATAGAGAGCGCTGAACCATGAACATTATGATGCAAAATACGTAAT 422

QY 1335 GGTTCGTTACCGACAACATTTGATATCCACCTTTGACATTTTTCACCACTCTTCCCGCCGA 1394

DB 423 TAATGCGATCCCTCCGACCTTGACTGCCAAGATTCACTTCAGACCAGAGCTTCCAGCAGA 482

QY 1395 GA 1396

DB 483 GA 484

RESULT 11

US-10-044-090-86

; Sequence 86, Application US/10044090

; Patent No. US20020137081A1

; GENERAL INFORMATION:

; APPLICANT: Olga Bandman

; TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION

; FILE REFERENCE: PA-0028 US

; CURRENT APPLICATION NUMBER: US/10/044,090

; CURRENT FILING DATE: 2002-01-09

; NUMBER OF SEQ ID NOS: 850

; SOFTWARE: PERL Program

; SEQ ID NO 86

; LENGTH: 4024

; TYPE: DNA

; ORGANISM: Homo sapiens


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Best Local Similarity 50.0%; Pred. No. 2;
Matches 85; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

QY 379 GATGCCACGGCGCTGGTGCCAGGACACTCGACCCCGACAGCAACGTTGGGACGCTGGTAGTG 438
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Db 1359 GGTGCGCTGGCGTTGGGCCGCGAGCGCTTGAGCGCCTTCGCTTCGCCGGCGAGCTGCTG 1418

QY 439 GTGGGCGCTGGCTTGAGCGGTTTGAGAGCGGACGCAAGTCCAGGCCCGCGCTCTGTCC 498
      |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 1419 CTGGTCTGGGATGATCATCTTGCCTGGTGGTGTGTCAGCTGTATCGGCGGCGCGCCG 1478

QY 499 TGCTCGTTCTTCAGCGCATGATCGTGTAGGGGGAAGACTCTGACCGT 548
      |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 1479 AGCTGGACCCGCGCGCTCGGCGCTGTGGCGCCTGGGCGCTGCTCTT 1528

RESULT 15
US-09-795-668-1008
; Sequence 1008, Application US/09795668
; Patent No. US20020045577A1
; GENERAL INFORMATION:
; APPLICANT: Stefansson, Hreinn
; APPLICANT: Steinthorsdottir, Valgerdur
; APPLICANT: Calcher, Jeffrey R.
; TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
; FILE REFERENCE: 2345.2004-001
; CURRENT APPLICATION NUMBER: US/09/795,668
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 09/515,716
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 1531
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1008
; LENGTH: 401
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-795-668-1008

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GenCore version 5.1.3
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Perfect score: 1929
Sequence: 1 atggcacttgaccagagcta.....gctctgtgccagcatag 1929

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 2 | 1827 | 94.7 | 1929 | 6 | ARI45465 Sequence |
| 3 | 324 | 16.8 | 1389 | 6 | ARI45447 Sequence |
| 4 | 324 | 16.8 | 1389 | 6 | ARI45474 Sequence |
| 5 | 324 | 16.8 | 1392 | 6 | ARI45449 Sequence |
| 6 | 324 | 16.8 | 1392 | 6 | ARI45476 Sequence |
| 7 | 324 | 16.8 | 1442 | 6 | ARI45448 Sequence |
| 8 | 324 | 16.8 | 1442 | 6 | ARI45475 Sequence |
| 9 | 324 | 16.8 | 1464 | 6 | ARI45456 Sequence |
| 10 | 324 | 16.8 | 1464 | 6 | ARI45483 Sequence |
| 11 | 324 | 16.8 | 1673 | 6 | ARI45454 Sequence |
| 12 | 324 | 16.8 | 1673 | 6 | ARI45481 Sequence |
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| 14 | 324 | 16.8 | 1803 | 6 | ARI45484 Sequence |
| 15 | 324 | 16.8 | 1930 | 6 | ARI45466 Sequence |
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| 21 | 324 | 16.8 | 2976 | 6 | ARI45486 Sequence |
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| 23 | 324 | 16.8 | 3003 | 6 | ARI45485 Sequence |
| 24 | 324 | 16.8 | 3591 | 6 | ARI45461 Sequence |
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| 26 | 324 | 16.8 | 3618 | 6 | ARI45460 Sequence |
| 27 | 324 | 16.8 | 3618 | 6 | ARI45487 Sequence |
| 28 | 167 | 8.7 | 1928 | 6 | ARI45467 Sequence |
| 29 | 167 | 8.7 | 1928 | 6 | ARI45468 Sequence |
| 30 | 165 | 8.6 | 1928 | 6 | ARI45469 Sequence |
| 31 | 124 | 6.4 | 372 | 6 | ARI45443 Sequence |
| 32 | 124 | 6.4 | 372 | 6 | ARI45470 Sequence |
| 33 | 75 | 3.9 | 182 | 6 | ARI45444 Sequence |
| 34 | 75 | 3.9 | 182 | 6 | ARI45471 Sequence |
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| 36 | 28 | 1.5 | 28 | 6 | ARI45453 Sequence |
| 37 | 28 | 1.5 | 28 | 6 | ARI45473 Sequence |
| 38 | 28 | 1.5 | 28 | 6 | ARI45480 Sequence |
| 39 | 28 | 1.5 | 37 | 6 | ARI45463 Sequence |
| 40 | 23 | 1.2 | 34 | 6 | ARI45450 Sequence |
| 41 | 23 | 1.2 | 34 | 6 | ARI45451 Sequence |
| 42 | 23 | 1.2 | 34 | 6 | ARI45477 Sequence |
| 43 | 23 | 1.2 | 34 | 6 | ARI45478 Sequence |
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| 45 | 21 | 1.1 | 137152 | 2 | AF004564 Oryza sat |

ALIGNMENTS

RESULT 1
ARI45464
LOCUS ARI45464 1929 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 35 from patent US 6211434.
ACCESSION ARI45464
VERSION ARI45464.1 GI:15107331
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1929)
AUTHORS Davick,J.P., Gilliam,J.T. and Maddox,J.R.
TITLE Amino polyol amine oxidase polynucleotides and related polypeptides and methods of use
JOURNAL Patent: US 6211434-A 35 03-APR-2001;

| FEATURES | | | | Location/Qualifiers | | | |
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| source | | | | 1..1929 | | | |
| BASE COUNT | | | | 451 a 537 c 532 g 409 t | | | |
| ORIGIN | | | | | | | |
| Query Match | | | | 100.0%; Score 1929; DB 6; Length 1929; | | | |
| Best Local Similarity | | | | 100.0%; Pred. No. 0; | | | |
| Matches 1929; Conservative | | | | 0; Mismatches 0; Indels 0; Gaps 0; | | | |
| QY | 1 | ATGGCAGTTCACCGAGCTACATCAATCCCAACAGCTGCCTCCCAAGAGGGTATTC | 60 | | | | |
| Db | 1 | ATGGCACTTGCACCGAGCTACATCAATCCCAACAGCTGCCTCCCAAGAGGGTATTC | 60 | | | | |
| QY | 61 | CACATCGGGTAGGCCCAACCAAGCAGGATATGACAATAGCTGGACAGATTGGACAA | 120 | | | | |
| Db | 61 | CACATCGGGTAGGCCCAACCAAGCAGGATATGACAATAGCTGGACAGATTGGACAA | 120 | | | | |
| QY | 121 | GACGCTTTGGCGGTGACAGACCCAGCCTACGAGAAACAGGTTGCCCAAGCATTCGCCAAT | 180 | | | | |
| Db | 121 | GACGCTTTGGCGGTGACAGACCCAGCCTACGAGAAACAGGTTGCCCAAGCATTCGCCAAT | 180 | | | | |
| QY | 181 | CTGCGAGCTTGGCTTGTCTGACGTTGGAGCCTCTTCAAAACGAGCTCACCAGCTCAATTTAC | 240 | | | | |
| Db | 181 | CTGCGAGCTTGGCTTGTCTGACGTTGGAGCCTCTTCAAAACGAGCTCACCAGCTCAATTTAC | 240 | | | | |
| QY | 241 | TACATCGTCGACTACGCCCGGAGCAAACTACCGCAATTGGAGATGGGTGAAGTCTACCT | 300 | | | | |
| Db | 241 | TACATCGTCGACTACGCCCGGAGCAAACTACCGCAATTGGAGATGGGTGAAGTCTACCT | 300 | | | | |
| QY | 301 | TTTGGCCCTTGACAGGTCCTCTTGCAGCTTGGTGCAGTACCAGGCTTGGCTTCACT | 360 | | | | |
| Db | 301 | TTTGGCCCTTGACAGGTCCTCTTGCAGCTTGGTGCAGTACCAGGCTTGGCTTCACT | 360 | | | | |
| QY | 361 | GAATACCTTTGAGGTTGATCCAGCGGCTTGGTGCAGGATGGATCGTGTAGGGGGAAGACT | 420 | | | | |
| Db | 361 | GAATACCTTTGAGGTTGATCCAGCGGCTTGGTGCAGGATGGATCGTGTAGGGGGAAGACT | 420 | | | | |
| QY | 421 | GTTGCGAGGTGATGTTGGCGGTGCTTGGAGCGGTTTGGAGACGCGACGCAAAATC | 480 | | | | |
| Db | 421 | GTTGCGAGGTGATGTTGGCGGTGCTTGGAGCGGTTTGGAGACGCGACGCAAAATC | 480 | | | | |
| QY | 481 | CAGCGCGCGGCTGTCTTGCCTCTTGGAGCGATGGATCGTGTAGGGGGAAGACT | 540 | | | | |
| Db | 481 | CAGCGCGCGGCTGTCTTGCCTCTTGGAGCGATGGATCGTGTAGGGGGAAGACT | 540 | | | | |
| QY | 541 | CTGAGGTACAAATCGGGTCCCGCAGGACGACTATCAACGACCTCGGCGTGGTGGATC | 600 | | | | |
| Db | 541 | CTGAGGTACAAATCGGGTCCCGCAGGACGACTATCAACGACCTCGGCGTGGTGGATC | 600 | | | | |
| QY | 601 | AATGACAGCAACAAAGCGAAGTATCCAGATTGTTTGAAGATTTCATTTGAGGGCGGAG | 660 | | | | |
| Db | 601 | AATGACAGCAACAAAGCGAAGTATCCAGATTGTTTGAAGATTTCATTTGAGGGCGGAG | 660 | | | | |
| QY | 661 | CTCCAGGACGACCGGAATTCATCCATCAAGCAAGAGCGGTACACCACTACAGCT | 720 | | | | |
| Db | 661 | CTCCAGGACGACCGGAATTCATCCATCAAGCAAGAGCGGTACACCACTACAGCT | 720 | | | | |
| QY | 721 | CTTTATGTTGACTCCCGGTAAAGCAATCCCACTTTGTGATGAGACCTCTCTGCGAGTGT | 780 | | | | |
| Db | 721 | CTTTATGTTGACTCCCGGTAAAGCAATCCCACTTTGTGATGAGACCTCTCTGCGAGTGT | 780 | | | | |
| QY | 781 | AGAAATACAGTCACTGACTTCAGTTCAGCTGATCGAAGAGTATAGCTTTGAAGACCCCAAGC | 840 | | | | |
| Db | 781 | AGAAATACAGTCACTGACTTCAGTTCAGCTGATCGAAGAGTATAGCTTTGAAGACCCCAAGC | 840 | | | | |
| QY | 841 | GGAACCTCTCCCGTATGTTCTCAGCTGATCGAAGAGTATAGCTTTGAAGACCCCAAGC | 900 | | | | |
| Db | 841 | GGAACCTCTCCCGTATGTTCTCAGCTGATCGAAGAGTATAGCTTTGAAGACCCCAAGC | 900 | | | | |
| QY | 901 | GAGCCCTCAGGCGAAGCGGCTGCACAGTGTGAGCTTTCGCGCACTACTGTGAGAAGGACCT | 960 | | | | |
| Db | 901 | GAGCCCTCAGGCGAAGCGGCTGCACAGTGTGAGCTTTCGCGCACTACTGTGAGAAGGACCT | 960 | | | | |

RESULT 2
AR145465
LOCUS

1929 bp DNA linear PAT 08-AUG-2001

DEFINITION Sequence 37 from patent US 6211434.
ACCESSION ARI45465
VERSION ARI45465.1 GI:15107332
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1929)
AUTHORS Duwick,J.P., Gilliam,J.T. and Maddox,J.R.
TITLE Amino polyol amine oxidase polynucleotides and related polypeptides
and methods of use
JOURNAL Patent: US 6211434-A 37 03-APR-2001;
FEATURES Location/Qualifiers
1..1929
source /organism="unknown"
BASE COUNT 451 a 539 c 532 g 407 t
ORIGIN

Query Match 94.7%; Score 1827; DB 6; Length 1929;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1927; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGCAGCTTGACCGAGCTACATCAATCCCAACAGCTCGCCTCCCAGCAGGGTATTCC 60
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QY 61 CACATCGCGTAGGCCCCAAAGCGAGGTATGTGACAAATAGCTGGACAGATTGGACAA 120
DB 61 CACATCGCGTAGGCCCCAAAGCGAGGTATGTGACAAATAGCTGGACAGATTGGACAA 120

QY 121 GACGCTTTGGCGGTGACAGACCCAGCCTACGAGAAACAGGTTGCCAAGCATTCGCCAAT 180
DB 121 GACGCTTTGGCGGTGACAGACCCAGCCTACGAGAAACAGGTTGCCAAGCATTCGCCAAT 180

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QY 301 TTGCGCCTTGACAGCTCCCTCCCTTGACAGCTGGTGGCCAGTACCGGCGTTGGCTTACCT 360
DB 301 TTGCGCCTTGACAGCTCCCTCCCTTGACAGCTGGTGGCCAGTACCGGCGTTGGCTTACCT 360

QY 361 GAATACCTCTTTGAGGTTGATGCCACGCGCTGGTGGCCAGCACACTCGACCCAGACAAC 420
DB 361 GAATACCTCTTTGAGGTTGATGCCACGCGCTGGTGGCCAGCACACTCGACCCAGACAAC 420

QY 421 GTTCGGACGTGGTAGTGGTGGCGCTGGCTTGAGCGGTTTGAGAGCGGCACCAAGTC 480
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QY 481 CAGCGCGCGGTCTGCTCGCTGCTTCTGAGCGATGATCGTGTAGGGGGAAGAGCT 540
DB 481 CAGCGCGCGGTCTGCTCGCTGCTTCTGAGCGATGATCGTGTAGGGGGAAGAGCT 540

QY 541 CTGAGCTACAAATCGGTGCCGAGGACGACTATCAACGACCTCGCGCTGGCTGGATC 600
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QY 781 AGAATACAGTCACTGACTCOACTTCCTCAGCTGAGCGAGGAGTTGCAAGTGCACCTGC 840
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DB 1141 CGGTGCTCTCAGGTAGGGACTCGTTTCTTAGTGGTCAATCCAGGTATGAGTGCATT 1200

QY 1201 TGCATGCCATGTCACAAAGCAACTTGTTCAGGCTCAGTGCACCTCAACACCCCGCTCGCT 1260
DB 1201 TGCATGCCATGTCACAAAGCAACTTGTTCAGGCTCAGTGCACCTCAACACCCCGCTCGCT 1260

QY 1261 GGAATGAGAGTGGCGCTCGGCTGTATAGTACGATCGGCTCGGGCGCTGTTCGGA 1320
DB 1261 GGAATGAGAGTGGCGCTCGGCTGTATAGTACGATCGGCTCGGGCGCTGTTCGGA 1320

QY 1321 AGCAAAAGGTGGTGGTTTGTACCGACAACATGTATCCACCTTGACATTTTCAACA 1380
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DB 1381 CTTCTTCCCGCGAGAAAGCAATTTGGCGAAAATCTATCTCGGCTACTATAGCAAG 1440

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QY 1561 TCCATTACCTGTTTCAATGTCGAGACCGGAGCGGAAAGTGGTCCCAACAGTCCAAAGCAG 1620
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QY 1681 GTCCAGAGCCCGCAAGCTGCTCGAAATCGAGTGGTCCGAGCAGCAGTATTTCCAAGA 1740
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QY 1801 CGGTTCAAGTGTTCATTCGTTGAGGAGCGCTCTTTAGTTTGGAAAGGTTATATG 1860
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QY 1861 GAAGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAAGTTGTGGCTAGCCTGGTGCCA 1920
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Db 1861 GAAGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAAGTTGTGGCTAGCCTGGTGCCA 1920
QY 1921 GCAGCATAG 1929
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Db 1921 GCAGCATAG 1929

RESULT 3
AR145447
LOCUS AR145447 1389 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 5 from patent US 6211434.
ACCESSION AR145447
VERSION AR145447.1 GI:15107314
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 1389)
AUTHORS Duvick,J.P., Gilliam,J.T. and Maddox,J.R.
TITLE Amino polyol amine oxidase polynucleotides and related polypeptides
and methods of use
JOURNAL Patent: US 6211434-A 5 03-APR-2001;
FEATURES Location/Qualifiers
source 1..1389
BASE COUNT 332 a 370 c 395 g 292 t
ORIGIN

Query Match 16.8%; Score 324; DB 6; Length 1389;
Best Local Similarity 99.7%; Pred. No. 4.6e-168;
Matches 374; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1615 AAGCAGGTACGACAAAAGTCTGTCTGGGACCAACTCCGCGACGCTACGAGAACGCCGGG 1674
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Db 1075 AAGCAGGTACGACAAAAGTCTGTCTGGGACCAACTCCGCGACGCTACGAGAACGCCGGG 1134
QY 1675 GCCCAAGTCCGAGAGCCGCAACGCTGCTCGAATCGAGTGGTCCGAGCAGCAGTATTC 1734
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Db 1135 GCCCAAGTCCGAGAGCCGCAACGCTGCTCGAATCGAGTGGTCCGAGCAGCAGTATTC 1194
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QY 1795 AGAAGCGGTTCAAGTGTGTTTCATTTCTGGGAACGAGACGCTTTTAGTTTGAAGGG 1854
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QY 1855 TATATGAAGGGCCATACGATCGGTCACGAGGTCTCAGAAAGTTGTGGCTAGCCTG 1914
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Db 1315 TATATGAAGGGCCATACGATCGGTCACGAGGTCTCAGAAAGTTGTGGCTAGCCTG 1374
QY 1915 GTGCCAGCAGCATAG 1929
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Db 1375 GTGCCAGCAGCATAG 1389

RESULT 5
AR145449
LOCUS AR145449 1392 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 10 from patent US 6211434.
ACCESSION AR145449
VERSION AR145449.1 GI:15107316
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 1392)
AUTHORS Duvick,J.P., Gilliam,J.T. and Maddox,J.R.
TITLE Amino polyol amine oxidase polynucleotides and related polypeptides
and methods of use
JOURNAL Patent: US 6211434-A 10 03-APR-2001;
FEATURES Location/Qualifiers
source 1..1392
BASE COUNT 335 a 370 c 395 g 292 t
ORIGIN

Query Match 16.8%; Score 324; DB 6; Length 1392;
Best Local Similarity 99.7%; Pred. No. 4.6e-168;
Matches 374; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1555 CAATGTCCATTACCTGTTTCATGTCGGAGACCCGGGACGGAAGTGGTCCCAACAGTCC 1614
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Db 1018 CAATGTCCATTACCTGTTTCATGTCGGAGACCCGGGACGGAAGTGGTCCCAACAGTCC 1077

QY 1861 GAAGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAAGTTGTGGCTAGCCTGGTGCCA 1920
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Db 1861 GAAGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAAGTTGTGGCTAGCCTGGTGCCA 1920
QY 1921 GCAGCATAG 1929
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Db 1921 GCAGCATAG 1929

RESULT 3
AR145447
LOCUS AR145447 1389 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 5 from patent US 6211434.
ACCESSION AR145447
VERSION AR145447.1 GI:15107314
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 1389)
AUTHORS Duvick,J.P., Gilliam,J.T. and Maddox,J.R.
TITLE Amino polyol amine oxidase polynucleotides and related polypeptides
and methods of use
JOURNAL Patent: US 6211434-A 5 03-APR-2001;
FEATURES Location/Qualifiers
source 1..1389
BASE COUNT 332 a 370 c 395 g 292 t
ORIGIN

Query Match 16.8%; Score 324; DB 6; Length 1389;
Best Local Similarity 99.7%; Pred. No. 4.6e-168;
Matches 374; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1555 CAATGTCCATTACCTGTTTCATGTCGGAGACCCGGGACGGAAGTGGTCCCAACAGTCC 1614
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Db 1015 CAATGTCCATTACCTGTTTCATGTCGGAGACCCGGGACGGAAGTGGTCCCAACAGTCC 1074
QY 1615 AAGCAGGTACGACAAAAGTCTGTCTGGGACCAACTCCGCGACGCTACGAGAACGCCGGG 1674
|||||
Db 1075 AAGCAGGTACGACAAAAGTCTGTCTGGGACCAACTCCGCGACGCTACGAGAACGCCGGG 1134
QY 1675 GCCCAAGTCCGAGAGCCGCAACGCTGCTCGAATCGAGTGGTCCGAGCAGCAGTATTC 1734
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Db 1135 GCCCAAGTCCGAGAGCCGCAACGCTGCTCGAATCGAGTGGTCCGAGCAGCAGTATTC 1194
QY 1735 CAAGGAGCTCCGAGCGCGCTATATGGGCTGAACGATCTCATCAGTGGTTCGGGCGTC 1794
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Db 1195 CAAGGAGCTCCGAGCGCGCTATATGGGCTGAACGATCTCATCAGTGGTTCGGGCGTC 1254
QY 1795 AGAAGCGGTTCAAGTGTGTTTCATTTCTGGGAACGAGACGCTTTTAGTTTGAAGGG 1854
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Db 1255 AGAAGCGGTTCAAGTGTGTTTCATTTCTGGGAACGAGACGCTTTTAGTTTGAAGGG 1314
QY 1855 TATATGAAGGGCCATACGATCGGTCACGAGGTCTCAGAAAGTTGTGGCTAGCCTG 1914
|||||
Db 1315 TATATGAAGGGCCATACGATCGGTCACGAGGTCTCAGAAAGTTGTGGCTAGCCTG 1374
QY 1915 GTGCCAGCAGCATAG 1929
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Db 1375 GTGCCAGCAGCATAG 1389

RESULT 4
AR145474
LOCUS AR145474 1389 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 5 from patent US 6211435.
ACCESSION AR145474
VERSION AR145474.1 GI:15107341
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

QY 1615 AAGCAGGTACGACAAAAGTCTCTCTGGGACCAACTCCCGCGCAGCCTACGAGAACGCCGGG 1674
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 Db 1198 CAAGGAGCTCCGAGCGCCGCTCTATGGCTGAACGATCTCATCACACTGGGTTCCGGCGCTC 1257
 QY 1795 AGAACGCCGTTCAAGTGTGTTTCAATTCCTGTTGGAACGAGCAGCTTTTGTGGAAGG 1854
 Db 1258 AGAACGCCGTTCAAGTGTGTTTCAATTCCTGTTGGAACGAGCAGCTTTTGTGGAAGG 1317
 QY 1855 TATATGAAGGGCCATACGATCGGTGCTCAACGAGGTGCTGCAAGAGTGTGGCTAGCCTG 1914
 Db 1318 TATATGAAGGGCCATACGATCGGTGCTCAACGAGGTGCTGCAAGAGTGTGGCTAGCCTG 1377
 QY 1915 GTGCCAGCAGCATAG 1929
 Db 1378 GTGCCAGCAGCATAG 1392
 RESULT 6
 ARI145476
 LOCUS ARI145476 1392 bp DNA linear PAT 08-AUG-2001
 DEFINITION Sequence 10 from patent US 6211435.
 ACCESSION ARI145476
 VERSION ARI145476.1 GI:15107343
 KEYWORDS .
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 1392)
 AUTHORS Duvick,J.P., Gilliam,J.T., Maddox,J.R., Crasta,O.R. and Folkerts,O.
 TITLE Amino polyol amine oxidase polynucleotides and related polypeptides
 and methods of use
 JOURNAL Patent: US 6211435-A 10 03-APR-2001;
 FEATURES Location/Qualifiers
 source 1..1392
 BASE COUNT 335 a 370 c 395 g 292 t
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 Best Local Similarity 99.7%; Pred. No. 4.6e-168;
 Matches 374; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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 Db 1018 CAATGGTCCATTACCTGTTTCATGGTCCGAGACCCGGGACGGAAGTGTCCCAACAGTCC 1077
 QY 1615 AAGCAGGTACGACAAAAGTCTCTCTGGGACCAACTCCCGCGCAGCCTACGAGAACGCCGGG 1674
 Db 1078 AAGCAGGTACGACAAAAGTCTCTCTGGGACCAACTCCCGCGCAGCCTACGAGAACGCCGGG 1137
 QY 1675 GCCCAAGTCCGAGCGCGCCACGCTGCTGGAATCGAGTGTGGAAGCAGCAGTATTTC 1734
 Db 1138 GCCCAAGTCCGAGCGCGCCACGCTGCTGGAATCGAGTGTGGAAGCAGCAGTATTTC 1197
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 QY 1795 AGAACGCCGTTCAAGTGTGTTTCAATTCCTGTTGGAACGAGCAGCTTTTGTGGAAGG 1854
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 Db 1318 TATATGAAGGGCCATACGATCGGTGCTCAACGAGGTGCTGCAAGAGTGTGGCTAGCCTG 1377

QY 1915 GTGCCAGCAGCATAG 1929
 Db 1378 GTGCCAGCAGCATAG 1392
 RESULT 7
 ARI145448
 LOCUS ARI145448 1442 bp DNA linear PAT 08-AUG-2001
 DEFINITION Sequence 7 from patent US 6211434.
 ACCESSION ARI145448
 VERSION ARI145448.1 GI:15107315
 KEYWORDS .
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 1442)
 AUTHORS Duvick,J.P., Gilliam,J.T. and Maddox,J.R.
 TITLE Amino polyol amine oxidase polynucleotides and related polypeptides
 and methods of use
 JOURNAL Patent: US 6211434-A 7 03-APR-2001;
 FEATURES Location/Qualifiers
 source 1..1442
 BASE COUNT 336 a 381 c 416 g 309 t
 ORIGIN-
 Query Match 16.8%; Score 324; DB 6; Length 1442;
 Best Local Similarity 99.7%; Pred. No. 4.6e-168;
 Matches 374; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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 QY 1855 TATATGAAGGGCCATACGATCGGTGCTCAACGAGGTGCTGCAAGAGTGTGGCTAGCCTG 1914
 Db 1368 TATATGAAGGGCCATACGATCGGTGCTCAACGAGGTGCTGCAAGAGTGTGGCTAGCCTG 1427
 QY 1915 GTGCCAGCAGCATAG 1929
 Db 1428 GTGCCAGCAGCATAG 1442
 RESULT 8
 ARI145475
 LOCUS ARI145475 1442 bp DNA linear PAT 08-AUG-2001
 DEFINITION Sequence 7 from patent US 6211435.
 ACCESSION ARI145475
 VERSION ARI145475.1 GI:15107342
 KEYWORDS .
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 1442)
 AUTHORS Duvick,J.P., Gilliam,J.T., Maddox,J.R., Crasta,O.R. and Folkerts,O.
 TITLE Amino polyol amine oxidase polynucleotides and related polypeptides

| | |
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| and methods of use | |
| JOURNAL | Patent: US 6211435-A 7 03-APR-2001; |
| FEATURES | Location/Qualifiers |
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| BASE COUNT | 336 a 381 c 416 g 309 t |
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| QY 1615 | AAGCAGGTACGACAAAGTCTCTCTGGACCAACTCCGCGCAGGCTACGAGAACGCCGGG 1674 |
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| QY 1675 | GCCCAAGTCCCAGAGCCGCCAACGTGCTCGAAATCGAGTGGTGAAGCAGCAGTATTTC 1734 |
| Db 1188 | GCCCAAGTCCCAGAGCCGCCAACGTGCTCGAAATCGAGTGGTGAAGCAGCAGTATTTC 1247 |
| QY 1735 | CAAGAGCTCCGAGGCCGCTCTATGGGTGAACGATCTCATCACACTGGGTTGGCGCTC 1794 |
| Db 1248 | CAAGAGCTCCGAGGCCGCTCTATGGGTGAACGATCTCATCACACTGGGTTGGCGCTC 1307 |
| QY 1795 | AGAACGCCGTTCAAGTGTGTTTCATTTCTGGAGCGAGAGCTCTTTAGTTTGAAGGG 1854 |
| Db 1308 | AGAACGCCGTTCAAGTGTGTTTCATTTCTGGAGCGAGAGCTCTTTAGTTTGAAGGG 1367 |
| QY 1855 | TATATGGAAGGGCCATACGATCGGGTCAACGAGGTGCTCGAGAAGTTGTGGCTAGCCTG 1914 |
| Db 1368 | TATATGGAAGGGCCATACGATCGGGTCAACGAGGTGCTCGAGAAGTTGTGGCTAGCCTG 1427 |
| QY 1915 | GTGCCAGCAGCATAG 1929 |
| Db 1428 | GTGCCAGCAGCATAG 1442 |
| RESULT 9 | |
| ARI45456 | |
| LOCUS | ARI45456 1464 bp DNA linear PAT 08-AUG-2001 |
| DEFINITION | Sequence 20 from patent US 6211434. |
| ACCESSION | ARI45456 |
| VERSION | ARI45456.1 GI:15107323 |
| KEYWORDS | Unknown. |
| SOURCE | Unknown. |
| ORGANISM | Unclassified. |
| REFERENCE | 1 (bases 1 to 1464) |
| AUTHORS | Duwick,J.P., Gilliam,J.T. and Maddox,J.R. |
| TITLE | Amino polyol amine oxidase polynucleotides and related polypeptides and methods of use |
| JOURNAL | Patent: US 6211434-A 20 03-APR-2001; |
| FEATURES | Location/Qualifiers |
| source | 1. .1464 |
| BASE COUNT | 343 a 405 c 409 g 307 t |
| ORIGIN | /organism="unknown" |
| Query Match | |
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| Matches 374; | Conservative 0; Mismatches 1; Indels 0; Gaps 0; |
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| QY 1615 | AGCAGGTACGACAAAGTCTCTCTGGGACCAACTCCGCGCAGCCTACGAGAACGCCGGG 1674 |
| Db 1150 | AGCAGGTACGACAAAGTCTCTCTGGGACCAACTCCGCGCAGCCTACGAGAACGCCGGG 1209 |
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| Db 1210 | GCCCAAGTCCCAGAGCCGCCAACGTGCTCGAAATCGAGTGGTGAAGCAGCAGTATTTC 1269 |
| QY 1735 | CAAGAGCTCCGAGGCCGCTCTATGGGTGAACGATCTCATCACACTGGGTTGGCGCTC 1794 |
| Db 1270 | CAAGAGCTCCGAGGCCGCTCTATGGGTGAACGATCTCATCACACTGGGTTGGCGCTC 1329 |
| QY 1795 | AGAAGCCGCTTCAAGTGTGTTTCATTTCTGGAACGGAGAGCTCTTTAGTTTGAAGGG 1854 |
| Db 1330 | AGAAGCCGCTTCAAGTGTGTTTCATTTCTGGAACGGAGAGCTCTTTAGTTTGAAGGG 1389 |
| QY 1855 | TATATGGAAGGGCCATACGATCGGGTCAACGAGGTGCTCGAGAAGTTGTGGCTAGCCTG 1914 |
| Db 1390 | TATATGGAAGGGCCATACGATCGGGTCAACGAGGTGCTCGAGAAGTTGTGGCTAGCCTG 1449 |
| QY 1915 | GTGCCAGCAGCATAG 1929 |
| Db 1450 | GTGCCAGCAGCATAG 1464 |
| RESULT 10 | |
| ARI45483 | |
| LOCUS | ARI45483 1464 bp DNA linear PAT 08-AUG-2001 |
| DEFINITION | Sequence 20 from patent US 6211435. |
| ACCESSION | ARI45483 |
| VERSION | ARI45483.1 GI:15107350 |
| KEYWORDS | Unknown. |
| SOURCE | Unknown. |
| ORGANISM | Unclassified. |
| REFERENCE | 1 (bases 1 to 1464) |
| AUTHORS | Duwick,J.P., Gilliam,J.T., Maddox,J.R., Crasta,O.R. and Folkerts,O. |
| TITLE | Amino polyol amine oxidase polynucleotides and related polypeptides and methods of use |
| JOURNAL | Patent: US 6211435-A 20 03-APR-2001; |
| FEATURES | Location/Qualifiers |
| source | 1. .1464 |
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| ORIGIN | /organism="unknown" |
| Query Match | |
| Best Local Similarity | 16.8%; Score 324; DB 6; Length 1464; |
| Matches 374; | Conservative 0; Mismatches 1; Indels 0; Gaps 0; |
| QY 1555 | CAATGTCATTACCTGTTTCATGTCGGAGACCCGGGACCGGAAGTGTCCCAACAGTCC 1614 |
| Db 1090 | CAATGTCATTACCTGTTTCATGTCGGAGACCCGGGACCGGAAGTGTCCCAACAGTCC 1149 |
| QY 1615 | AGCAGGTACGACAAAGTCTCTCTGGGACCAACTCCGCGCAGCCTACGAGAACGCCGGG 1674 |
| Db 1150 | AGCAGGTACGACAAAGTCTCTCTGGGACCAACTCCGCGCAGCCTACGAGAACGCCGGG 1209 |
| QY 1675 | GCCCAAGTCCCAGAGCCGCCAACGTGCTCGAAATCGAGTGGTGAAGCAGCAGTATTTC 1734 |
| Db 1210 | GCCCAAGTCCCAGAGCCGCCAACGTGCTCGAAATCGAGTGGTGAAGCAGCAGTATTTC 1269 |
| QY 1735 | CAAGAGCTCCGAGGCCGCTCTATGGGTGAACGATCTCATCACACTGGGTTGGCGCTC 1794 |
| Db 1270 | CAAGAGCTCCGAGGCCGCTCTATGGGTGAACGATCTCATCACACTGGGTTGGCGCTC 1329 |
| QY 1795 | AGAAGCCGCTTCAAGTGTGTTTCATTTCTGGAACGGAGAGCTCTTTAGTTTGAAGGG 1854 |
| Db 1330 | AGAAGCCGCTTCAAGTGTGTTTCATTTCTGGAACGGAGAGCTCTTTAGTTTGAAGGG 1389 |
| QY 1855 | TATATGGAAGGGCCATACGATCGGGTCAACGAGGTGCTCGAGAAGTTGTGGCTAGCCTG 1914 |
| Db 1390 | TATATGGAAGGGCCATACGATCGGGTCAACGAGGTGCTCGAGAAGTTGTGGCTAGCCTG 1449 |
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| Db 1450 | GTGCCAGCAGCATAG 1464 |

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QY 1735 CAAGGAGCTCCGAGCGCGCTATGGCTGAACGATCTCATCACACTGGGTTCCGGCGCTC 1794

Db 1609 CAAAGAGCTCCGAGCGCGCTATGGCTGAACGATCTCATCACACTGGGTTCCGGCGCTC 1668

QY 1795 AGAACCGCGTTCAAGTGTGTTTCATTTCTGTTGGAACGAGACGCTCTTTAGTTTGGAAAGG 1854

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QY 1855 TATATGGAAGGGCCATACGATCGGTTCAACGAGTGTCTCGAAGTGTGGCTAGCCTG 1914

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QY 1915 GTGCCAGCAGCATAG 1929

Db 1789 GTGCCAGCAGCATAG 1803

RESULT 14

ARI45484

LOCUS ARI45484 1803 bp DNA linear PAT 08-AUG-2001

DEFINITION Sequence 22 from patent US 6211435.

ACCESSION ARI45484

VERSION ARI45484.1 GI:15107351

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 1803)

AUTHORS Duvick,J.P., Gilliam,J.T., Maddox,J.R., Crasta,O.R. and Folkerts,O.

TITLE Amino polyol amine oxidase polynucleotides and related polypeptides and methods of use

JOURNAL Patent: US 6211435-A 22 03-APR-2001;

FEATURES

source Location/Qualifiers

1..1803

BASE COUNT 424 a 501 c 502 g 376 t

ORIGIN

Query Match 16.8%; Score 324; DB 6; Length 1803;

Best Local Similarity 99.7%; Pred. No. 4.5e-168;

Matches 374; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1555 CAATGGTCCATTACCTGTTTCATGTCGGAGACCCGGGACGGAAGTGGTCCCAACAGTCC 1614

Db 1429 CAATGGTCCATTACCTGTTTCATGTCGGAGACCCGGGACGGAAGTGGTCCCAACAGTCC 1488

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QY 1795 AGAACCGCGTTCAAGTGTGTTTCATTTCTGTTGGAACGAGACGCTCTTTAGTTTGGAAAGG 1854

Db 1669 AGAACCGCGTTCAAGAGTGTTCATTTCTGTTGGAACGAGACGCTCTTTAGTTTGGAAAGG 1728

QY 1855 TATATGGAAGGGCCATACGATCGGTTCAACGAGTGTCTCGAAGTGTGGCTAGCCTG 1914

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QY 1915 GTGCCAGCAGCATAG 1929

Db 1789 GTGCCAGCAGCATAG 1803

RESULT 15

ARI45466

LOCUS ARI45466 1930 bp DNA linear PAT 08-AUG-2001

DEFINITION Sequence 39 from patent US 6211434.

ACCESSION ARI45466

VERSION ARI45466.1 GI:15107333

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 1930)

AUTHORS Duvick,J.P., Gilliam,J.T. and Maddox,J.R.

TITLE Amino polyol amine oxidase polynucleotides and related polypeptides and methods of use

JOURNAL Patent: US 6211434-A 39 03-APR-2001;

FEATURES

source Location/Qualifiers

1..1930

BASE COUNT 449 a 551 c 537 g 412 t 1 others

ORIGIN

Query Match 16.8%; Score 324; DB 6; Length 1930;

Best Local Similarity 99.7%; Pred. No. 4.5e-168;

Matches 374; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1615 AAGCAGGTACGACAAAGTCTGTCTGGGACCAACTCCGCGCAGCCTACGAGAACGCCGG 1674

Db 1616 AAGCAGGTACGACAAAGTCTGTCTGGGACCAACTCCGCGCAGCCTACGAGAACGCCGG 1675

QY 1675 GCCCAAGTCCCAGAGCGCGCCCAAGCTGCTCGAAATCGAGTGGTCTGGAAGCAGCATATTTTC 1734

Db 1676 GCCCAAGTCCCAGAGCGCGCCCAAGCTGCTCGAAATCGAGTGGTCTGGAAGCAGCATATTTTC 1735

QY 1735 CAAGGAGCTCCGAGCGCGCTATGGCTGAACGATCTCATCACACTGGGTTCCGGCGCTC 1794

Db 1736 CAAGGAGCTCCGAGCGCGCTATGGCTGAACGATCTCATCACACTGGGTTCCGGCGCTC 1795

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Db 1796 AGAACCGCGTTCAAGAGTGTTCATTTCTGTTGGAACGAGACGCTCTTTAGTTTGGAAAGG 1855

QY 1855 TATATGGAAGGGCCATACGATCGGTTCAACGAGTGTCTCGAAGTGTGGCTAGCCTG 1914

Db 1856 TATATGGAAGGGCCATACGATCGGTTCAACGAGTGTCTCGAAGTGTGGCTAGCCTG 1915

QY 1915 GTGCCAGCAGCATAG 1929

Db 1916 GTGCCAGCAGCATAG 1930

Search completed: November 12, 2002, 07:53:50

Job time : 5088 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 12, 2002, 03:23:20 ; Search time 417 Seconds
(without alignments)
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Perfect score: 1929
Sequence: 1 atdgacttgaccagagcta.....gctctgtgcccagcatag 1929

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 1125999159 residues

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Minimum DB seq length: 0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 4 | 324 | 16.8 | 1389 | 21 | AAZ60630 |
| 5 | 324 | 16.8 | 1392 | 21 | AAZ58394 |
| 6 | 324 | 16.8 | 1392 | 21 | AAZ60633 |
| 7 | 324 | 16.8 | 1442 | 21 | AAZ58393 |
| 8 | 324 | 16.8 | 1442 | 21 | AAZ60631 |
| 9 | 324 | 16.8 | 1464 | 21 | AAZ58401 |
| | | | | | Exophiala spinifer |
| | | | | | Exophiala spinifer |
| | | | | | Amino polyol amine |
| | | | | | DNA encoding an am |
| | | | | | Amino polyol amine |
| | | | | | DNA encoding an am |
| | | | | | Amino polyol amine |
| | | | | | DNA encoding an am |

| | | | | | | |
|----|-----|------|------|----|----------|---------------------|
| 10 | 324 | 16.8 | 1464 | 21 | AAZ60640 | DNA encoding an am |
| 11 | 324 | 16.8 | 1673 | 21 | AAZ58395 | Amino polyol amine |
| 12 | 324 | 16.8 | 1673 | 21 | AAZ60638 | Exophiala spinifer |
| 13 | 324 | 16.8 | 1803 | 21 | AAZ58402 | Exophiala spinifer |
| 14 | 324 | 16.8 | 1803 | 21 | AAZ60641 | DNA encoding a ful |
| 15 | 324 | 16.8 | 1930 | 21 | AAZ58384 | Exophiala spinifer |
| 16 | 324 | 16.8 | 2079 | 21 | AAZ58400 | DNA encoding GST-t |
| 17 | 324 | 16.8 | 2079 | 21 | AAZ60639 | DNA encoding an am |
| 18 | 324 | 16.8 | 2490 | 21 | AAZ58407 | DNA encoding GST-t |
| 19 | 324 | 16.8 | 2490 | 21 | AAZ60646 | DNA encoding a fus |
| 20 | 324 | 16.8 | 2976 | 21 | AAZ58404 | DNA encoding funon |
| 21 | 324 | 16.8 | 2976 | 21 | AAZ60643 | DNA encoding a fus |
| 22 | 324 | 16.8 | 3003 | 21 | AAZ58403 | DNA encoding funon |
| 23 | 324 | 16.8 | 3003 | 21 | AAZ60642 | DNA encoding a fus |
| 24 | 324 | 16.8 | 3591 | 21 | AAZ58406 | DNA encoding funon |
| 25 | 324 | 16.8 | 3591 | 21 | AAZ60645 | DNA encoding a fus |
| 26 | 324 | 16.8 | 3618 | 21 | AAZ58405 | DNA encoding funon |
| 27 | 324 | 16.8 | 3618 | 21 | AAZ60644 | DNA encoding a fus |
| 28 | 167 | 8.7 | 1928 | 21 | AAZ58385 | Rhinocladiaella atr |
| 29 | 167 | 8.7 | 1928 | 21 | AAZ58386 | Rhinocladiaella atr |
| 30 | 165 | 8.6 | 1928 | 21 | AAZ58387 | Rhinocladiaella atr |
| 31 | 124 | 6.4 | 372 | 21 | AAZ58388 | Exophiala spinifer |
| 32 | 124 | 6.4 | 372 | 21 | AAZ60664 | Nucleotide sequenc |
| 33 | 75 | 3.9 | 182 | 21 | AAZ58389 | Exophiala spinifer |
| 34 | 75 | 3.9 | 182 | 21 | AAZ60663 | Nucleotide sequenc |
| 35 | 28 | 1.5 | 28 | 21 | AAZ58391 | Primer N21988 used |
| 36 | 28 | 1.5 | 28 | 21 | AAZ58399 | Amino polyol amine |
| 37 | 28 | 1.5 | 28 | 21 | AAZ60629 | 5' RACE primer use |
| 38 | 28 | 1.5 | 28 | 21 | AAZ60637 | PCR primer N21968 |
| 39 | 28 | 1.5 | 37 | 21 | AAZ58408 | Primer 23294 desi |
| 40 | 23 | 1.2 | 34 | 21 | AAZ58396 | Primer N23256 desi |
| 41 | 23 | 1.2 | 34 | 21 | AAZ58397 | Primer N23259 desi |
| 42 | 23 | 1.2 | 34 | 21 | AAZ60634 | PCR primer N23256 |
| 43 | 23 | 1.2 | 34 | 21 | AAZ60635 | PCR primer N23259 |
| 44 | 20 | 1.0 | 5990 | 22 | AAK67673 | Human immune/haema |
| 45 | 20 | 1.0 | 6118 | 23 | ABL07290 | Drosophila melanog |

ALIGNMENTS

| | |
|----------|---|
| RESULT 1 | |
| AAZ58382 | |
| ID | AAZ58382 standard; DNA; 1929 BP. |
| XX | |
| AC | AAZ58382; |
| XX | |
| DT | 23-MAY-2000 (first entry) |
| XX | |
| DE | Exophiala spinifera amino polyol amine oxidase ESP002_C2 DNA. |
| XX | |
| KW | Amino polyol amine oxidase; fumonisin; mycotoxin; transgenic plant; |
| KW | detoxification; animal feed; silage; selectable marker; ds. |
| XX | |
| OS | Exophiala spinifera. |
| XX | |
| EH | Key |
| FT | CDS |
| FT | Location/Qualifiers |
| FT | 1..1929 |
| FT | /*tag= a |
| FT | /note= "contains introns" |
| FT | 739..811 |
| FT | /*tag= b |
| FT | 1134..1186 |
| FT | /*tag= c |
| XX | |
| PN | WO200004159-A1. |
| XX | |
| PD | 27-JAN-2000. |
| XX | |
| PF | 08-JUL-1999; 99WO-US15454. |
| XX | |
| PR | 15-JUL-1998; 98US-0092936. |
| PR | 21-MAY-1999; 99US-0135391. |

XX (PION-) PIONEER HI-BRED INT INC.
PA (CURA-) CURAGEN CORP.
XX
PI DuVick JP, Gilliam JT, Maddox JR;
XX
DR WPI; 2000-182425/16.
XX P-PSDB; AAY58900.
XX
PT New isolated polynucleotides, polypeptides useful for detecting and
PT degrading fumonisin or structurally related mycotoxin in processed
PT grain or in silage
XX
XX Claim 1; Page 137-138; 154pp; English.
XX
XX The present sequence is that of an isolated nucleic acid,
CC designated ESP002.C2, of Exophiala spinifera isolate ESP002,
CC which encodes an amino polyol amine oxidase (APO, see AAY58900)
CC capable of degrading fumonisin, its hydrolysis product AP1, and
CC related mycotoxins. The DNA was obtained by PCR amplification of
CC ESP002 mycelial DNA using primers based on APO of E. spinifera
CC ATCC 74269. The invention provides APO polynucleotides (see
CC AAY58900-05) and polypeptides (see AAY58900-05) of E. spinifera and
CC Rhinocladella atrovirens. The polynucleotides are used to transform
CC plant cells normally susceptible to Fusarium or other toxin-producing
CC fungus infection. Transgenic plants can be regenerated from the
CC transformed plant cells. Also provided are methods for expressing
CC both APO and a fumonisin-esterase in a transgenic plant, and for
CC producing APO enzyme in prokaryotic and non-plant eukaryotic
CC systems. Transgenic plants capable of degrading fumonisin or of
CC producing the degrading enzymes are provided. Methods for
CC detoxification of grain, grain processing, silage, food crops and
CC in animal feed and rumen microorganisms are also disclosed. APO
CC polynucleotide is also useful as a selectable marker.
XX
SQ Sequence 1929 BP; 451 A; 537 G; 532 C; 409 T; 0 other;

Query Match 100.0%; Score 1929; DB 21; Length 1929;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1929; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCACTTGCACCGAGTACATCAATCCCCAAAGCTCGCTCCCGACGAGGTATTC 60
DB (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||)
DB 1 ATGGCACTTGCACCGAGTACATCAATCCCCAAAGCTCGCTCCCGACGAGGTATTC 60
QY 61 CACATCGGCGTAGGGCCCAACGAGCGAGGTATGCACAATAGCTGGACAGATTGGACAA 120
DB (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||)
DB 61 CACATCGGCGTAGGGCCCAACGAGCGAGGTATGCACAATAGCTGGACAGATTGGACAA 120
QY 121 GACGCTTTGGGCGTGACAGACCCAGCCTACGAGAACAGAGTTGGCCCAAGCTACGCCAAT 180
DB (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||)
DB 121 GACGCTTTGGGCGTGACAGACCCAGCCTACGAGAACAGAGTTGGCCCAAGCTACGCCAAT 180
QY 181 CTGCGAGCTTGCTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
DB (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||)
DB 181 CTGCGAGCTTGCTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240
QY 241 TACATCGTGGACTACGCCCGGAGCAACTCACCGCAATTTGGAGATGGGCTGAAGTCTAC 300
DB (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||)
DB 241 TACATCGTGGACTACGCCCGGAGCAACTCACCGCAATTTGGAGATGGGCTGAAGTCTAC 300
QY 301 TTTGCCCTTTGACAGGCTCCCTCTCTGACGCTGGTGCCAGTACCGGCTTGCTTCACCT 360
DB (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||)
DB 301 TTTGCCCTTTGACAGGCTCCCTCTCTGACGCTGGTGCCAGTACCGGCTTGCTTCACCT 360
QY 361 GATACCTCTTTGAGTTGATCCAGCGGCTGGTGCCAGGACCTCCGACCCACACAC 420
DB (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||)
DB 361 GATACCTCTTTGAGTTGATCCAGCGGCTGGTGCCAGGACCTCCGACCCACACAC 420
QY 421 GTTGGGAGCTGGTAGTGGGCGCTGGCTTTGAGCGTTTGGAGACGCGACGCAAGTC 480
DB (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||)
DB 421 GTTGGGAGCTGGTAGTGGGCGCTGGCTTTGAGCGTTTGGAGACGCGACGCAAGTC 480

QY 481 CAGCCGCCGCTCTGCTCCTCGCTCTGTTTGGAGCGATGATGCTGTTAGGGGAAAGACT 540
DB (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||)
DB 481 CAGCCGCCGCTCTGCTCCTCGCTCTGTTTGGAGCGATGATGCTGTTAGGGGAAAGACT 540
QY 541 CTGAGCGTACAATCGGGTCCCGCAGGAGACTATCAACGACCTCGGCGCTGGTGGATC 600
DB (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||)
DB 541 CTGAGCGTACAATCGGGTCCCGCAGGAGACTATCAACGACCTCGGCGCTGGTGGATC 600
QY 601 AATGACAGCAACCAAGCGAAGTATCCAGATTGTTTGAAGATTTCATTTGAGGGCGAG 660
DB (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||)
DB 601 AATGACAGCAACCAAGCGAAGTATCCAGATTGTTTGAAGATTTCATTTGAGGGCGAG 660
QY 661 CTCAGAGGACGACCGGAAATTCATCCATCAAGCAACAGCGGTACACCACTACAGCT 720
DB (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||)
DB 661 CTCAGAGGACGACCGGAAATTCATCCATCAAGCAACAGCGGTACACCACTACAGCT 720
QY 721 CCTTATGGTGAATCCCGGTAAGCAAACTCCACTTTGTGATGAGACCTCTCTCGAGTGT 780
DB (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||)
DB 721 CCTTATGGTGAATCCCGGTAAGCAAACTCCACTTTGTGATGAGACCTCTCTCGAGTGT 780
QY 781 AGAATACAGTCACTGACTCCACTTCGTCCAGCTGAGCGAGGAGTTGCAAGTGCACCTTC 840
DB (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||)
DB 781 AGAATACAGTCACTGACTCCACTTCGTCCAGCTGAGCGAGGAGTTGCAAGTGCACCTTC 840
QY 841 GGAATCTCTCCCGTATGCTGCTCAGCTGATGCGAAGAGTATAGCTTTGAAGACCCCAAGGC 900
DB (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||)
DB 841 GGAATCTCTCCCGTATGCTGCTCAGCTGATGCGAAGAGTATAGCTTTGAAGACCCCAAGGC 900
QY 901 GAGCCCTCAGGCGAAGCGGCTCGACAGTGTGAGCTTCGGGCACCTACTGTGAGAGACCT 960
DB (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||)
DB 901 GAGCCCTCAGGCGAAGCGGCTCGACAGTGTGAGCTTCGGGCACCTACTGTGAGAGACCT 960
QY 961 AAATCTCCCTGCTGCTTCTCAGCGTGGCAACACAGATCACACGCGCTCTGCTCGGTGGA 1020
DB (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||)
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QY 1021 AGCCACGAGATCAGATGCTTTTCTCAGCGTGTGAGCTTCGGGCACCTACTGTGAGAGACCT 1080
DB (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||)
DB 1021 AGCCACGAGATCAGATGCTTTTCTCAGCGTGTGAGCTTCGGGCACCTACTGTGAGAGACCT 1080
QY 1081 TAATATTGCTCTCGGACAAGAAAGACGGCGGAGTATATCGGATGCAAAACAGAGTGGCTG 1140
DB (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||)
DB 1081 TAATATTGCTCTCGGACAAGAAAGACGGCGGAGTATATCGGATGCAAAACAGAGTGGCTG 1140
QY 1141 CGGTGCTCTCTCAGGTAGGGAGTCTGTTCTTAGTGGTCAATCCAGGTATGCAAGTGCAGTT 1200
DB (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||)
DB 1141 CGGTGCTCTCTCAGGTAGGGAGTCTGTTCTTAGTGGTCAATCCAGGTATGCAAGTGCAGTT 1200
QY 1201 TGCCATGCCATGTCAAGAGAACTTTTCCAGGCTCAGTGCAACCTCAACACCCCGCTCGCT 1260
DB (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||)
DB 1201 TGCCATGCCATGTCAAGAGAACTTTTCCAGGCTCAGTGCAACCTCAACACCCCGCTCGCT 1260
QY 1261 GGAATTCAGCAGTCCGGCTCCGGCTGTATAGTACGATCGGCTCGGCGCGCTGTTTCCGA 1320
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DB 1261 GGAATTCAGCAGTCCGGCTCCGGCTGTATAGTACGATCGGCTCGGCGCGCTGTTTCCGA 1320
QY 1321 AGCAAAAGGTGGTGGTTCGTTTACCAGCAACATTTGATCCCACTTGACATTTTCAACA 1380
DB (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||)
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QY 1381 CCTCTTCCCGCGAGAGCAAGCATTTGGCGGAAATCTATCTCGGCTACTATAGCAAG 1440
DB (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||)
DB 1381 CCTCTTCCCGCGAGAGCAAGCATTTGGCGGAAATCTATCTCGGCTACTATAGCAAG 1440
QY 1441 ATAGTCTTCGATGGGACAAACCCGTTGGTGGCGGAAACAGGCTTCTCGGCGCTCTCCAA 1500
DB (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||) (|||||)
DB 1441 ATAGTCTTCGATGGGACAAACCCGTTGGTGGCGGAAACAGGCTTCTCGGCGCTCTCCAA 1500
QY 1501 TCGAGCTGTGACCCCATCTCATTTGCCAGAGATACCAAGATCGAAGTCGATCGCGAATGG 1560
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Db 1561 TCCATTACCTGTTTCATGGTCGGAGACCCGGACGGAAGTGGTCCACACATCCAAAGCAG 1620
QY 1621 GTACGACAAAAGTCTGTGGACCAACTCCGCGCAGCCTACGAGAACGCCGGGGCCCAA 1680
Db 1621 GTACGACAAAAGTCTGTGGACCAACTCCGCGCAGCCTACGAGAACGCCGGGGCCCAA 1680
QY 1681 GTCCAGAGCGCGCCAACTGCTCGAAATCGAGTGGTCTGAAAGCAGCAGTATTTCCAAAGGA 1740
Db 1681 GTCCAGAGCGCGCCAACTGCTCGAAATCGAGTGGTCTGAAAGCAGCAGTATTTCCAAAGGA 1740
QY 1741 GTCGAGCGCGCTATGGGCTGAACGATCTCATACACTGGGTTGGCGCTCAGAACG 1800
Db 1741 GTCGAGCGCGCTATGGGCTGAACGATCTCATACACTGGGTTGGCGCTCAGAACG 1800
QY 1801 CGGTTCAAGTGTTCATTTGCTTGAACGAGAGCTCTTTAGTTTGAAGGCTATATG 1860
Db 1801 CGGTTCAAGTGTTCATTTGCTTGAACGAGAGCTCTTTAGTTTGAAGGCTATATG 1860
QY 1861 GAAGGGCCATACGATCGGCTCAAGAGTGTCTGAGAAAGTGTGGCTAGCTGTGCCA 1920
Db 1861 GAAGGGCCATACGATCGGCTCAAGAGTGTCTGAGAAAGTGTGGCTAGCTGTGCCA 1920
QY 1921 GCAGCATAG 1929
Db 1921 GCAGCATAG 1929

RESULT 2
AAZ58383
ID AAZ58383 standard; DNA; 1929 BP.
XX
AC AAZ58383;
XX
DT 23-MAY-2000 (first entry)
XX
DE Exophiala spinifera amino polyol amine oxidase ESP002_C3 DNA.
XX
KW Amino polyol amine oxidase; fumonisins; mycotoxin; transgenic plant;
KW detoxification; animal feed; silage; selectable marker; ds.
XX
OS Exophiala spinifera.
XX
FH Key Location/Qualifiers
FT CDS 1..1929
FT /*tag= a
FT /*note= "contains introns"
FT intron 739..811
FT /*tag= b
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XX
PN WO200004159-A1.
XX
PD 27-JAN-2000.
XX
PF 08-JUL-1999; 99WO-US15454.
XX
PR 15-JUL-1998; 98US-0092936.
PR 21-MAY-1999; 99US-0135391.
XX
PA (PION-) PIONEER HI-BRED INT INC.
PA (CURA-) CURAGEN CORP.
XX
PI Duvick JP, Gilliam JT, Maddox JR;
XX
XX WPI; 2000-182425/16.
DR P-PSDB; AAY58901.
XX
XX New isolated polynucleotides, polypeptides useful for detecting and
PT degrading fumonisins or structurally related mycotoxin in processed
PT grain or in silage
XX

PS Claim 1; Page 139-140; 154pp; English.
XX
CC The present sequence is that of an isolated nucleic acid.
CC designated ESP002_C3 of Exophiala spinifera isolate ESP002.
CC which encodes an amino polyol amine oxidase (APAO, see AAY58901)
CC capable of degrading fumonisins, its hydrolysis product API, and
CC related mycotoxins. The DNA was obtained by PCR amplification of
CC ESP002 mycelial DNA using primers based on APAO of E. spinifera
CC ATCC 74269. The invention provides APAO polynucleotides (see
CC AAZ58383-87) and polypeptides (see AAY58900-05) of E. spinifera and
CC rhinocardiella atrovirens. The polynucleotides are used to transform
CC plant cells normally susceptible to Fusarium or other toxin-producing
CC fungus infection. Transgenic plants can be regenerated from the
CC transformed plant cells. Also provided are methods for expressing
CC both APAO and a fumonisin-esterase in a transgenic plant, and for
CC producing APAO enzyme in prokaryotic and non-plant eukaryotic
CC systems. Transgenic plants capable of degrading fumonisins or of
CC producing the degrading enzymes are provided. Methods for
CC detoxification of grain, grain processing, silage, food crops and
CC in animal feed and rumen microorganisms are also disclosed. APAO
CC polynucleotide is also useful as a selectable marker.
XX
SQ Sequence 1929 BP; 451 A; 539 C; 532 G; 407 T; 0 other;
Query Match 94.7%; Score 1827; DB 21; Length 1929;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1927; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ATGGCAGCTTGCACCGAGCTACATCAATCCCCCAAGAGTGCCTCCCGCAGGAGGTATCC 60
Db 1 ATGGCAGCTTGCACCGAGCTACATCAATCCCCCAAGAGTGCCTCCCGCAGGAGGTATCC 60
QY 61 CACATCGCGCTAGGCGCCAAACGAAGCGAGGTATGTGACAAATAGCTGGACAGATTGGACAA 120
Db 61 CACATCGCGCTAGGCGCCAAACGAAGCGAGGTATGTGACAAATAGCTGGACAGATTGGACAA 120
QY 121 GAGCGCTTTGGCGGTGACAGACCGCCTACGAGAAACAGGTTGCCCAAGCATTCGCAAT 180
Db 121 GAGCGCTTTGGCGGTGACAGACCGCCTACGAGAAACAGGTTGCCCAAGCATTCGCAAT 180
QY 181 CTGGGAGCTTGGCTTGCCTGCTGAGTGGAGCCTCTTCAACGACGTCCACCAAGCTCAATTAC 240
Db 181 CTGGGAGCTTGGCTTGCCTGCTGAGTGGAGCCTCTTCAACGACGTCCACCAAGCTCAATTAC 240
QY 241 TACATCGTGCAGTACGCCCGGAGCAAACTCACCGCAATTGGAGATGGGTGAAGTCTACC 300
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QY 301 TTGCGCCTTGACAGGCTCCCTCTTGCACGCTGGTGCCAGTACCGGCTTGGCTTCACCT 360
Db 301 TTGCGCCTTGACAGGCTCCCTCTTGCACGCTGGTGCCAGTACCGGCTTGGCTTCACCT 360
QY 361 GAATACCTCTTTGAGTTGATGCCACGGCGCTGGTCCAGGACACTCGACCCGAGACAAC 420
Db 361 GAATACCTCTTTGAGTTGATGCCACGGCGCTGGTCCAGGACACTCGACCCGAGACAAC 420
QY 421 GTTGGCAGCTGGTGTAGTGGTGGCGCTTGGAGCGTTGGAGACGGCACCACCAAGTC 480
Db 421 GTTGGCAGCTGGTGTAGTGGTGGCGCTTGGAGCGTTGGAGACGGCACCACCAAGTC 480
QY 481 CAGCGCGCGCTCTGTCTCCCTCGCTTCTTGGAGCGGATGGATCGTGTAGGGGAAAGACT 540
Db 481 CAGCGCGCGCTCTGTCTCCCTCGCTTCTTGGAGCGGATGGATCGTGTAGGGGAAAGACT 540
QY 541 CTGAGCGTACAATCGGCTCCCGGAGGACGACTATCAACGACCTCGCGCTGGCTGATC 600
Db 541 CTGAGCGTACAATCGGCTCCCGGAGGACGACTATCAACGACCTCGCGCTGGCTGATC 600
QY 601 AATGACAGCAACCAAGCGAGTATCCAGATTGTTTCAGAGATTTCATTTGGAGGCGGAG 660
Db 601 AATGACAGCAACCAAGCGAGTATCCAGATTGTTTCAGAGATTTCATTTGGAGGCGGAG 660
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Db 661 CTTCCAGAGACGACCGAAATTCATCCATCAAGCACAGACGGTACAACCACTACAGCT 720
QY 721 CTTATGGTGACTCCCGGTAAAGCAATCCACATTTGTGATGAGACCTCTGTCAAGTGT 780
Db 721 CTTATGGTGACTCCCGGTAAAGCAATCCACATTTGTGATGAGACCTCTGTCAAGTGT 780
QY 781 AGAATACAGTCACTGACTCCACTTCGTCCAGCTGAGCGAGGAGTGTGAAGTGCACTTGC 840
Db 781 AGAATACAGTCACTGACTCCACTTCGTCCAGCTGAGCGAGGAGTGTGAAGTGCACTTGC 840
QY 841 GGAATCTCTCCCGGTATGTCTAGCTGATGAAAGAGTATAGCCTTGAAGACCCCAAGGC 900
Db 841 GGAATCTCTCCCGGTATGTCTAGCTGATGAAAGAGTATAGCCTTGAAGACCCCAAGGC 900
QY 901 GAGCCCTCAGGCGAAGCGGCTCGACAGTGTGAGCTTCGCGCACTACTGTGAGAGGACCT 960
Db 901 GAGCCCTCAGGCGAAGCGGCTCGACAGTGTGAGCTTCGCGCACTACTGTGAGAGGACCT 960
QY 961 AAATTTGCCCTGTCTCAGCGTGGCAACCAAGATCACACGCGCTCTGCTCGGTGTGGA 1020
Db 961 AAATTTGCCCTGTCTCAGCGTGGCAACCAAGATCACACGCGCTCTGCTCGGTGTGGA 1020
QY 1021 AGCCACAGAGATCAGATGCTTTTCTCACCGACTACATCAAGAGTGCACCGGTCTCAG 1080
Db 1021 AGCCACAGAGATCAGATGCTTTTCTCACCGACTACATCAAGAGTGCACCGGTCTCAG 1080
QY 1081 TAATATTTCTCGGACAGAAAGCGGGCAGTATATGCGATCAAAACAGTGCCTG 1140
Db 1081 TAATATTTCTCGGACAGAAAGCGGGCAGTATATGCGATCAAAACAGTGCCTG 1140
QY 1141 CGGTGTCTCTCAGGTAGGGGACTGTTTCTTAGTGGTCAATCCAGGTATGAGTCGATT 1200
Db 1141 CGGTGTCTCTCAGGTAGGGGACTGTTTCTTAGTGGTCAATCCAGGTATGAGTCGATT 1200
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Db 1201 TGCATGCCATGTCAAAGAACTTGTTCAGGCTCAGTGCACCTCAACCCCGTCTCCT 1260
QY 1261 GGAATTTGAGCAGTCGGCGTCCGGCTGTAGTACCATCGGCTCGGCGCGGTCTCCGA 1320
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Db 1321 AGCAAAAGGTGGTGGTTTCTGTTACCGAACATTTGTATCCACCTTGACATTTTCACCA 1380
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Db 1381 CCTCTTCCCGCGAGACGACATTTGGGGAATAATCTATCCTGGCTACTATAGCAAG 1440
QY 1441 ATAGTCTTGTATGGCAACCCGTTGGCGCGAACAGGCTTCTCGGGCTCTCCAA 1500
Db 1441 ATAGTCTTGTATGGCAACCCGTTGGCGCGAACAGGCTTCTCGGGCTCTCCAA 1500
QY 1501 TCGAGTGTGACCCCATCTCATTTGCCAGAGATACCATCGAAGTGCATCGGCAATGG 1560
Db 1501 TCGAGTGTGACCCCATCTCATTTGCCAGAGATACCATCGAAGTGCATCGGCAATGG 1560
QY 1561 TCCATTACCTGTTTCATGGTGGAGACCCGGAGGAGTGGTCCCAACAGTCCCAAGCAG 1620
Db 1561 TCCATTACCTGTTTCATGGTGGAGACCCGGAGGAGTGGTCCCAACAGTCCCAAGCAG 1620
QY 1621 GTACGACAAAAGTCTGTCTGGGACCAACTCCGCGAGCTACGAGAACGCCGGGCCCAA 1680
Db 1621 GTACGACAAAAGTCTGTCTGGGACCAACTCCGCGAGCCTACGAGAACGCCGGGCCCAA 1680
QY 1681 GTCCAGAGCCGGCCAACTGCTCGAAATCGAGTGGTGGAGAGCAGTATTTCCAAAGGA 1740
Db 1681 GTCCAGAGCCGGCCAACTGCTCGAAATCGAGTGGTGGAGAGCAGTATTTCCAAAGGA 1740
QY 1741 GCTCCGAGCGCGCTATGGGCTGACCAATCTCATCACATGGGTTCGGCGCTCAGAACG 1800
Db 1741 GCTCCGAGCGCGCTATGGGCTGACCAATCTCATCACATGGGTTCGGCGCTCAGAACG 1800

Db 1741 GCTCCGAGCGCGCTATGGGCTGAACGATCTCATCACATGGGTTCGGCGCTCAGAACG 1800
QY 1801 CCGTTCAAGTGTGTTTCATTTCTGTTGGAAACGAGACGTCTTTAGTTTGGAAAGGTTATG 1860
Db 1801 CCGTTCAAGTGTGTTTCATTTCTGTTGGAAACGAGACGTCTTTAGTTTGGAAAGGTTATG 1860
QY 1861 GAAGGGCCCATACCATCGGTCAACGAGGTGCTGCAGAACTTGTGGCTACGCTGGTCCCA 1920
Db 1861 GAAGGGCCCATACCATCGGTCAACGAGGTGCTGCAGAACTTGTGGCTACGCTGGTCCCA 1920
QY 1921 GCAGCATAG 1929
Db 1921 GCAGCATAG 1929
RESULT 3
ID AAZ58392 standard; cDNA; 1389 BP.
XX AAZ58392;
XX AC AAZ58392;
XX AC AAZ58392;
DT 23-MAY-2000 (first entry)
XX Amino polyol amine oxidase truncated DNA k0n0-395_6.5.
DE Amino polyol amine oxidase; funonisin; mycotoxin; transgenic plant;
XX Amino polyol amine oxidase; funonisin; mycotoxin; transgenic plant;
KW detoxification; animal feed; silage; selectable marker; ss.
XX Exophiala spinifera.
OS Exophiala spinifera.
XX WO200004159-A1.
XX 27-JAN-2000.
XX 08-JUL-1999; 99WO-US15454.
XX 15-JUL-1998; 98US-0092936.
XX 21-MAY-1999; 99US-0135391.
XX (PION-) PIONEER HI-BRED INT INC.
XX (CURA-) CURAGEN CORP.
XX Duwick JP, Gilliam JT, Maddox JR;
XX WPI: 2000-182425/16.
XX P-PSDB; AAY58906.
XX New isolated polynucleotides, polypeptides useful for detecting and
PT degrading funonisin or structurally related mycotoxin in processed
PT grain or in silage -
XX Example 6; Page 74-76; 154pp; English.
XX The present sequence is that of polynucleotide k0n0-395_6.5, which
CC encodes a truncated, but still functional, amino polyol amine oxidase
CC (APAO, see AAY58906). The polynucleotide was obtained by 3' and 5'
CC RACE PCR using k0n0-395_5 (see AAZ58388), a partial APAO cDNA of
CC Exophiala spinifera. APAO is capable of degrading funonisin, its
CC hydrolysis product API and related mycotoxins. The invention
CC provides APAO polynucleotides (see AAZ58383-87) and polypeptides (see
CC AAY58900-05) of E. spinifera and Rhinocladia atrovirens. The
CC polynucleotides are used to transform plant cells normally
CC susceptible to Fusarium or other toxin-producing fungus infection.
CC Also provided are methods for expressing APAO in transgenic plants,
CC prokaryotic and non-plant eukaryotic systems. Methods for
CC detoxification of grain, grain processing, silage, food crops and
CC in animal feed and rumen microorganisms are also disclosed. APAO
CC polynucleotide can also be used as a selectable marker.
XX Sequence 1389 BP; 332 A; 370 C; 395 G; 292 T; 0 other;
SQ Query Match 16.8%; Score 324; DB 21; Length 1389;
Best Local similarity 99.7%; Pred. No. 1.8e-158;

Matches 374; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1555 CAATGTCATTACCTGTTTCATGTCGGAGACCGCGGAGAACTGCTCCACAGTCC 1614
|||||
Db 1015 CAATGTCATTACCTGTTTCATGTCGGAGACCGCGGAGAACTGCTCCACAGTCC 1074
QY 1615 AAGCAGGTACGACAAAGTCTCTGCGGACCAACTCCGCGAGCCTACGAGAACGCCGGG 1674
|||||
Db 1075 AAGCAGGTACGACAAAGTCTCTGCGGACCAACTCCGCGAGCCTACGAGAACGCCGGG 1134
QY 1675 GCCCAGTCCAGAGCGCGCAACTGCTCGAATCGAGTGTGCGAAGCAGATATTC 1734
|||||
Db 1135 GCCCAGTCCAGAGCGCGCAACTGCTCGAATCGAGTGTGCGAAGCAGATATTC 1194
QY 1735 CAAGAGTCCAGAGCGCGCTATGCGGTGAACGATCTCATCACACTGGTTCGCGCGTC 1794
|||||
Db 1195 CAAGAGTCCAGAGCGCGCTATGCGGTGAACGATCTCATCACACTGGTTCGCGCGTC 1254
QY 1795 AGAAGCGCTTCAAGTGTTCATTTCTGTTGGAACGGAGAGCTCTTTAGTTTGGAAAGG 1854
|||||
Db 1255 AGAAGCGCTTCAAGTGTTCATTTCTGTTGGAACGGAGAGCTCTTTAGTTTGGAAAGG 1314
QY 1855 TATATGGAAGGCGCATAGTCGGTCAACGAGTGTGCGAAGTGTGCGTAGCCTG 1914
|||||
Db 1315 TATATGGAAGGCGCATAGTCGGTCAACGAGTGTGCGAAGTGTGCGTAGCCTG 1374
QY 1915 GTGCCAGCAGCATAG 1929
|||||
Db 1375 GTGCCAGCAGCATAG 1389

RESULT 4
AAZ60630
ID AAZ60630 standard; DNA; 1389 BP.
XX
AC AAZ60630;
XX
DT 16-MAY-2000 (first entry)
XX
DE DNA encoding an aminopolylol amine oxidase clone trAPO.
XX
KW Aminopolylol amine oxidase; APO; mycotoxin degradation; antimicrobial;
KW plant fungal invasion; hydrogen peroxide; Fusarium; fungi; ss.
XX
OS Exophiala spinifera.
XX
FH Key Location/Qualifiers
FT CDS 1..1389
FT /*tag= a
FT /product= "aminopolylol amine oxidase"
XX
PN WO200004160-A1.
XX
PD 27-JAN-2000.
XX
PF 08-JUL-1999; 99WO-US15455.
XX
PR 15-JUL-1998; 98US-0092936.
XX
PA (PION-) PIONEER HI-BRED INT INC.
PA (CURA-) CURAGEN CORP.
XX
PI Crasta OR, Duvick J, Folkerts O, Gilliam JT, Maddox JR;
XX
DR WPI; 2000-182426/16.
DR P-PSDB; AAY68843.
XX
PT New nucleic acid encoding aminopolylol amine oxidase, used, e.g. to
PT generate plants resistant to Fusarium -
XX
PS Example 6; Page 75-77; 145pp; English.
XX
CC The present sequence encodes an Exophiala spinifera aminopolylol amine

CC oxidase (APO). The enzyme has homology to the flavin containing amine
CC oxidase family, that oxidise primary amine to an aldehyde or ketone,
CC releasing ammonia and hydrogen peroxide. The APO enzyme degrades
CC mycotoxins that promote fungal invasion of plants. Destruction of
CC mycotoxins by APO generates, as a by-product, hydrogen peroxide which
CC is itself an antimicrobial and stimulates the plants own defensive
CC systems. The APO polynucleotides are used to generate plants
CC (particularly maize) that are resistant to Fusarium or other fungi
CC that produce mycotoxins and/or to degrade such mycotoxins (e.g. during
CC ensiling); for recombinant production of APO polypeptides; as
CC selection markers for plant transformation; and to isolate related
CC sequences from other organisms. The APO polypeptides are used to
CC degrade mycotoxins in plant materials, including expression in
CC engineered bacteria and fungi, e.g. rumen microflora.
XX
SQ Sequence 1389 BP; 332 A; 370 C; 395 G; 292 T; 0 other;

Query Match 16.8%; Score 324; DB 21; Length 1389;
Best Local Similarity 99.7%; Pred. No. 1.8e-158;
Matches 374; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1555 CAATGTCATTACCTGTTTCATGTCGGAGACCGCGGAGAACTGCTCCACAGTCC 1614
|||||
Db 1015 CAATGTCATTACCTGTTTCATGTCGGAGACCGCGGAGAACTGCTCCACAGTCC 1074
QY 1615 AAGCAGGTACGACAAAGTCTCTGCGGACCAACTCCGCGAGCCTACGAGAACGCCGGG 1674
|||||
Db 1075 AAGCAGGTACGACAAAGTCTCTGCGGACCAACTCCGCGAGCCTACGAGAACGCCGGG 1134
QY 1675 GCCCAGTCCAGAGCGCGCAACTGCTCGAATCGAGTGTGCGAAGCAGATATTC 1734
|||||
Db 1135 GCCCAGTCCAGAGCGCGCAACTGCTCGAATCGAGTGTGCGAAGCAGATATTC 1194
QY 1735 CAAGAGTCCAGAGCGCGCTATGCGGTGAACGATCTCATCACACTGGTTCGCGCGTC 1794
|||||
Db 1195 CAAGAGTCCAGAGCGCGCTATGCGGTGAACGATCTCATCACACTGGTTCGCGCGTC 1254
QY 1795 AGAAGCGCTTCAAGTGTTCATTTCTGTTGGAACGGAGAGCTCTTTAGTTTGGAAAGG 1854
|||||
Db 1255 AGAAGCGCTTCAAGTGTTCATTTCTGTTGGAACGGAGAGCTCTTTAGTTTGGAAAGG 1314
QY 1855 TATATGGAAGGCGCATAGTCGGTCAACGAGTGTGCGAAGTGTGCGTAGCCTG 1914
|||||
Db 1315 TATATGGAAGGCGCATAGTCGGTCAACGAGTGTGCGAAGTGTGCGTAGCCTG 1374
QY 1915 GTGCCAGCAGCATAG 1929
|||||
Db 1375 GTGCCAGCAGCATAG 1389

RESULT 5
AAZ58394
ID AAZ58394 standard; cDNA; 1392 BP.
XX
AC AAZ58394;
XX
DT 23-MAY-2000 (first entry)
XX
DE Amino polyol amine oxidase DNA clone K:trAPO.
XX
KW Amino polyol amine oxidase; fumonisin; mycotoxin; transgenic plant;
KW detoxification; animal feed; silage; selectable marker; mutant; ss.
XX
OS Exophiala spinifera.
OS Synthetic.
XX
PN WO200004159-A1.
XX
PD 27-JAN-2000.
XX
PF 08-JUL-1999; 99WO-US15454.
XX
PR 15-JUL-1998; 98US-0092936.

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PR 21-MAY-1999; 99US-0135391.
XX
XX (PION-) PIONEER HI-BRED INT INC.
XX (CURA-) CURAGEN CORP.
XX
PI Duvick JP, Gilliam JT, Maddox JR;
XX
XX WPI; 2000-182425/16.
DR P-PSDB; AAY58909.
XX
XX New isolated polynucleotides, polypeptides useful for detecting and
PT degrading fumonisin or structurally related mycotoxin in processed
PT grain or in silage -
XX
XX Example 7; Page 81-83; 154pp; English.
XX
XX The present sequence is that of a polynucleotide encoded a truncated,
CC but still functional, amino polyol amine oxidase (K:trAPAO, see
CC AAY58909) of Exophiala spinifera. The polynucleotide was derived from
CC clone k0n0-395.6.5 (see AAY58392) to which was added a 5' lysine codon
CC (nucleotides 1-3), since many amine oxidases have a positively charged
CC amino acid near the N-terminus and upstream of a dinucleotide binding
CC site. The construct allowed heterologous expression of trAPAO in
CC Pichia pastoris and maize. The invention provides APAO polynucleotides
CC (see AAY58383-87) and polypeptides (see AAY58900-05) of E. spinifera and
CC Rhinocladia atrovirens. The polynucleotides are used to transform
CC plant cells normally susceptible to Fusarium or other toxin-producing
CC fungus infection. Also provided are methods for expressing APAO in
CC transgenic plants, prokaryotic and non-plant eukaryotic systems.
CC Methods for detoxification of grain, grain processing, silage, food
CC crops and in animal feed and rumen microorganisms are also disclosed.
CC APAO polynucleotide can also be used as a selectable marker.
XX
XX Sequence 1392 BP; 335 A; 370 C; 395 G; 292 T; 0 other;
SQ
Query Match 16.8%; Score 324; DB 21; Length 1392;
Best Local Similarity 99.7%; Pred. No. 1.8e-158;
Matches 374; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1555 CAATGGTCCATTACCTGTTTCATGTGCGAGACCCGGGACGGAAGTGGTCCCAACAGTCC 1614
DB 1018 CAATGGTCCATTACCTGTTTCATGTGCGAGACCCGGGACGGAAGTGGTCCCAACAGTCC 1077
QY 1615 AAGCAGGTACGACAAAAGTCTGTCTGGGACCAACTCCGGCGACGCTACGAGAACCCCGGG 1674
DB 1078 AAGCAGGTACGACAAAAGTCTGTCTGGGACCAACTCCGGCGACGCTACGAGAACCCCGGG 1137
QY 1675 GCCAAGTCCAGAGCGCGCCACGTCGTGCGAAATCGAGTGTGCGAAGCAGCATTTTC 1734
DB 1138 GCCAAGTCCAGAGCGCGCCACGTCGTGCGAAATCGAGTGTGCGAAGCAGCATTTTC 1197
QY 1735 CAAGGAGCTCCGAGCGCGCTCTATGGGCTGAACGATCTCATCACACTGGGTTTCGGCGCTC 1794
DB 1198 CAAGGAGCTCCGAGCGCGCTCTATGGGCTGAACGATCTCATCACACTGGGTTTCGGCGCTC 1257
QY 1795 AGAACGCCGTTCAAGTGTGTTTCATTTGCGTTGGAACGGAGACGCTTTAGTTTGGAAAGG 1854
DB 1258 AGAACGCCGTTCAAGTGTGTTTCATTTGCGTTGGAACGGAGACGCTTTAGTTTGGAAAGG 1317
QY 1855 TATATGGAAGGGCCATAGATCGGGTCAACGAGGTGCTGCAGAGATTTGCTGCTAGCCTG 1914
DB 1318 TATATGGAAGGGCCATAGATCGGGTCAACGAGGTGCTGCAGAGATTTGCTGCTAGCCTG 1377
QY 1915 GTGCCAGCAGCATAG 1929
DB 1378 GTGCCAGCAGCATAG 1392
RESULT 6
ID AA260633
XX AA260633 standard; DNA; 1392 BP.
AC AA260633;
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XX 16-MAY-2000 (first entry)
XX DNA encoding an aminopolylol amine oxidase clone K:trAPAO.
XX
XX Aminopolylol amine oxidase; APAO; mycotoxin degradation; antimicrobial;
XX plant fungal invasion; hydrogen peroxide; Fusarium; fungi; ss.
XX
XX Synthetic.
OS Exophiala spinifera.
XX
XX Key Location/Qualifiers
XX CDS 1..1392
XX FT /*tag= a
XX FT /product= "aminopolylol amine oxidase"
XX FT /note= "the amino terminal Lys was added to the
XX FT protein sequence for optimized expression"
XX
XX WC200004160-Al.
XX
XX 27-JAN-2000.
XX
XX 08-JUL-1999; 99WO-US15455.
XX
XX 15-JUL-1998; 98US-0092936.
XX
XX (PION-) PIONEER HI-BRED INT INC.
XX (CURA-) CURAGEN CORP.
XX
XX Crasta OR, Duvick J, Folkerts O, Gilliam JT, Maddox JR;
XX WPI; 2000-182426/16.
DR P-PSDB; AAY68845.
XX
XX New nucleic acid encoding aminopolylol amine oxidase, used, e.g. to
PT generate plants resistant to Fusarium -
XX
XX Example 7; Page 82-84; 145pp; English.
XX
XX The present sequence encodes an Exophiala spinifera aminopolylol amine
CC oxidase (APAO). The enzyme has homology to the flavin containing amine
CC oxidase family, that oxidise primary amine to an aldehyde or ketone,
CC releasing ammonia and hydrogen peroxide. The APAO enzyme degrades
CC mycotoxins that promote fungal invasion of plants. Destruction of
CC mycotoxins by APAO generates, as a by-product, hydrogen peroxide which
CC is itself an antimicrobial and stimulates the plants own defensive
CC systems. The APAO polynucleotides are used to generate plants
CC (particularly maize) that are resistant to Fusarium or other fungi
CC that produce mycotoxins and/or to degrade such mycotoxins (e.g. during
CC ensiling); for recombinant production of APAO polypeptides; as
CC selection markers for plant transformation; and to isolate related
CC sequences from other organisms. The APAO polypeptides are used to
CC degrade mycotoxins in plant materials, including expression in
CC engineered bacteria and fungi, e.g. rumen microflora.
XX
XX Sequence 1392 BP; 335 A; 370 C; 395 G; 292 T; 0 other;
SQ
Query Match 16.8%; Score 324; DB 21; Length 1392;
Best Local Similarity 99.7%; Pred. No. 1.8e-158;
Matches 374; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1555 CAATGGTCCATTACCTGTTTCATGTGCGAGACCCGGGACGGAAGTGGTCCCAACAGTCC 1614
DB 1018 CAATGGTCCATTACCTGTTTCATGTGCGAGACCCGGGACGGAAGTGGTCCCAACAGTCC 1077
QY 1615 AAGCAGGTACGACAAAAGTCTGTCTGGGACCAACTCCGGCGACGCTACGAGAACCCCGGG 1674
DB 1078 AAGCAGGTACGACAAAAGTCTGTCTGGGACCAACTCCGGCGACGCTACGAGAACCCCGGG 1137
QY 1675 GCCCAAGTCCAGAGCGCGCCACGTCGTGCGAAATCGAGTGTGCGAAGCAGCATTTTC 1734
DB 1138 GCCCAAGTCCAGAGCGCGCCACGTCGTGCGAAATCGAGTGTGCGAAGCAGCATTTTC 1197
```

QY 1735 CAAGGAGCTCCGAGCGCGTCTATGGCTGAACGATCTCATCACACTGGGTTCCGCGCTC 1794
|||||
Db 1198 CAAGGAGCTCCGAGCGCGTCTATGGCTGAACGATCTCATCACACTGGGTTCCGCGCTC 1257
|||||
QY 1795 AGAAGCGCGTTCAAGTGTTGTCATTTCCTTGGACGGAGAGCTCTTTAGTTGGAAAGGG 1854
|||||
Db 1258 AGAAGCGCGTTCAAGAGTGTTTCATTTCCTTGGACGGAGAGCTCTTTAGTTGGAAAGGG 1317
|||||
QY 1855 TATATGGAAGGGCCATACGATCGGGTCAACGAGTGCTGCGAGAAGTTGTGGCTAGCCTG 1914
|||||
Db 1318 TATATGGAAGGGCCATACGATCGGGTCAACGAGTGCTGCGAGAAGTTGTGGCTAGCCTG 1377
|||||
QY 1915 GTGCCAGCAGCATAG 1929
|||||
Db 1378 GTGCCAGCAGCATAG 1392
|||||
RESULT 7
AAZ58393
ID AAZ58393 standard; cDNA; 1442 BP.
XX
AC AAZ58393;
XX
DT 23-MAY-2000 (first entry)
XX
DE Amino polyol amine oxidase truncated DNA k0n0-395_5.4.
XX
KW Amino polyol amine oxidase; fumonisins; mycotoxin; transgenic plant;
KW detoxification; animal feed; silage; selectable marker; ss.
XX
OS Exophiala spinifera.
XX
FH Key Location/Qualifiers
FT CDS 1..1442
FT /*tag= a
FT /note= "contains an intron"
FT intron 647..699
FT /*tag= b
XX
PN WO200004159-A1.
XX
PD 27-JAN-2000.
XX
PF 08-JUL-1999; 99WO-US15454.
XX
PR 15-JUL-1998; 98US-0092936.
PR 21-MAY-1999; 99US-0135391.
XX
PA (PION-) PIONEER HI-BRED INT INC.
PA (CURA-) CURAGEN CORP.
XX
PI Duvick JP, Gilliam JT, Maddox JR;
XX
DR WPI; 2000-182425/16.
DR P-PSDB; AAY58907, AAY58908.
XX
PT New isolated polynucleotides, polypeptides useful for detecting and
PT degrading fumonisin or structurally related mycotoxin in processed
PT grain or in silage -
XX
PS Example 6; Page 77-79; 154pp; English.
XX
CC The present sequence is that of polynucleotide k0n0-395_5.4, which
CC encodes a truncated, but still functional, amino polyol amine oxidase
CC (trPAO-I, see AAY58907 and AAY58908). The polynucleotide was obtained
CC by 3' and 5' RACE PCR using k0n0-395.5 (see AAZ58388), a partial APAO
CC cDNA of Exophiala spinifera. APAO is capable of degrading fumonisin,
CC its hydrolysis product Ap1 and related mycotoxins. The invention
CC provides APAO polynucleotides (see AAZ58383-87) and polypeptides (see
CC AAY58900-05) of E. spinifera and Rhinocladiella atrovirens. The
CC polynucleotides are used to transform plant cells normally
CC susceptible to Fusarium or other toxin-producing fungus infection.
CC Also provided are methods for expressing APAO in transgenic plants,

CC prokaryotic and non-plant eukaryotic systems. Methods for
CC detoxification of grain, grain processing, silage, food crops and in
CC animal feed and rumen microorganisms are also disclosed. APAO
CC polynucleotide can also be used as a selectable marker.
XX
SQ Sequence 1442 BP; 336 A; 381 C; 416 G; 309 T; 0 other;
Query Match 16.8%; Score 324; DB 21; Length 1442;
Best Local Similarity 99.7%; Pred. No. 1.8e-158;
Matches 374; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1555 CAATGTGTCATTACCTGTTTCATGTCGGAGACCCGGGACCGGAAGTGTCCCAACAGTCC 1614
|||||
Db 1068 CAATGTGTCATTACCTGTTTCATGTCGGAGACCCGGGACCGGAAGTGTCCCAACAGTCC 1127
|||||
QY 1615 AAGCAGTAGCAGACAAAAGTCTGTCGGACCCTTCCGGCAGCCCTACGAGAACGCCGG 1674
|||||
Db 1128 AAGCAGTAGCAGACAAAAGTCTGTCGGACCCTTCCGGCAGCCCTACGAGAACGCCGG 1187
|||||
QY 1675 GCCCAAGTCCAGAGCGCGCAACGTGCTCGAAATCGAGTGTGCGAAGCAGCAGTATTC 1734
|||||
Db 1188 GCCCAAGTCCAGAGCGCGCAACGTGCTCGAAATCGAGTGTGCGAAGCAGCAGTATTC 1247
|||||
QY 1735 CAAGGAGCTCCGAGCGCGCTTATGGCTGAACGATCTCATCACACTGGGTTCCGCGCTC 1794
|||||
Db 1248 CAAGGAGCTCCGAGCGCGCTTATGGCTGAACGATCTCATCACACTGGGTTCCGCGCTC 1307
|||||
QY 1795 AGAAGCGCGTTCAAGTGTTGTCATTTCCTTGGACGGAGAGCTCTTTAGTTGGAAAGGG 1854
|||||
Db 1308 AGAAGCGCGTTCAAGAGTGTTTCATTTCCTTGGACGGAGAGCTCTTTAGTTGGAAAGGG 1367
|||||
QY 1855 TATATGGAAGGGCCATACGATCGGGTCAACGAGTGCTGCGAGAAGTTGTGGCTAGCCTG 1914
|||||
Db 1368 TATATGGAAGGGCCATACGATCGGGTCAACGAGTGCTGCGAGAAGTTGTGGCTAGCCTG 1427
|||||
QY 1915 GTGCCAGCAGCATAG 1929
|||||
Db 1428 GTGCCAGCAGCATAG 1442
|||||
RESULT 8
AAZ60631
ID AAZ60631 standard; DNA; 1442 BP.
XX
AC AAZ60631;
XX
DT 16-MAY-2000 (first entry)
XX
DE DNA encoding an aminopolyol amine oxidase clone trPAO-I.
XX
KW Aminopolyol amine oxidase; APAO; mycotoxin degradation; antimicrobial;
KW plant fungal invasion; hydrogen peroxide; Fusarium; fungi; ss.
XX
OS Exophiala spinifera.
XX
FH Key Location/Qualifiers
FT CDS 1..1442
FT /*tag= a
FT /product= "aminopolyol amine oxidase"
FT /note= "contains an intron"
FT exon 1..646
FT /*tag= b
FT /number= 1
FT intron 647..699
FT /*tag= c
FT /number= 1
FT exon 700..1439
FT /*tag= d
FT /number= 2
XX
XX WO200004160-A1.
XX
XX 27-JAN-2000.
PD

| | | | |
|--|--|--|------|
| PT | New nucleic acid encoding aminopolylol amine oxidase, used, e.g. to generate plants resistant to Fusarium | | |
| XX | Example 11; Page 95-97; 145pp; English. | | |
| PS | The present sequence encodes an Exophiala spinifera aminopolylol amine oxidase (APAO). The APAO enzyme has homology to the flavin containing amine oxidase family, that oxidise primary amine to an aldehyde or ketone, releasing ammonia and hydrogen peroxide. The APAO enzyme degrades mycotoxins that promote fungal invasion of plants. Destruction of mycotoxins by APAO generates, as a by-product, hydrogen peroxide which is itself an antimicrobial and stimulates the plants own defensive systems. The APAO polynucleotides are used to generate plants (particularly maize) that are resistant to Fusarium or other fungi that produce mycotoxins and/or to degrade such mycotoxins (e.g. during ensiling); for recombinant production of APAO polypeptides; as selection markers for plant transformation; and to isolate related sequences from other organisms. The APAO polypeptides are used to degrade mycotoxins in plant materials, including expression in engineered bacteria and fungi, e.g. rumen microflora. | | |
| XX | Sequence 1464 BP; 343 A; 405 C; 409 G; 307 T; 0 other; | | |
| Query Match 16.8%; Score 324; DB 21; Length 1464; Best Local Similarity 99.7%; Pred. No. 1.8e-158; Matches 374; Conservative 0; Mismatches 1; Indels 0; Gaps 0; | | | |
| QY | 1555 | CAATGGTCCATTACCTGTTTCATGTTGCGAGACCCGGGACGGAAGTGGTCCCAACAGTCC | 1614 |
| Db | 1090 | CAATGGTCCATTACCTGTTTCATGTTGCGAGACCCGGGACGGAAGTGGTCCCAACAGTCC | 1149 |
| QY | 1615 | AAGCAGGTACGACAAAGTCTGTCTGGGACCAACTCCGCGCAGCCTACGAGAACGCCGGG | 1674 |
| Db | 1150 | AAGCAGGTACGACAAAGTCTGTCTGGGACCAACTCCGCGCAGCCTACGAGAACGCCGGG | 1209 |
| QY | 1675 | GCCCAAGTCCAGAGCGCGGCGAAGTGTCTGAAATCGAGTGTCTGAAAGCAGTATTTTC | 1734 |
| Db | 1210 | GCCCAAGTCCAGAGCGCGGCGAAGTGTCTGAAATCGAGTGTCTGAAAGCAGTATTTTC | 1269 |
| QY | 1735 | CAAGGAGTCCGAGCGCGCTCTATGGGCTGAACGATCTCATCACATGCGGTTCGCGCGCTC | 1794 |
| Db | 1270 | CAAGGAGTCCGAGCGCGCTCTATGGGCTGAACGATCTCATCACATGCGGTTCGCGCGCTC | 1329 |
| QY | 1795 | AGAACGCCGTTCAAGTGTGTTTCATTTCTGTTGGAACGAGACGTCTTTAGTTTGGAAAGG | 1854 |
| Db | 1330 | AGAACGCCGTTCAAGAGTGTTCATTTCTGTTGGAACGAGACGTCTTTAGTTTGGAAAGG | 1389 |
| QY | 1855 | TATATGGAAGGGCCATACGATCGGTTCAACGAGGTGCTCGAAGTGTGTGGTACGCTG | 1914 |
| Db | 1390 | TATATGGAAGGGCCATACGATCGGTTCAACGAGGTGCTCGAAGTGTGTGGTACGCTG | 1449 |
| QY | 1915 | GTGCCAGCAGCATAG | 1929 |
| Db | 1450 | GTGCCAGCAGCATAG | 1464 |
| RESULT 11 AAZ58395 ID AAZ58395 standard; cDNA; 1673 BP. XX XX XX AAZ58395; XX DT 23-MAY-2000 (first entry) XX XX Amino polylol amine oxidase (alpha mating factor signal peptide) DNA. XX Amino polylol amine oxidase; APAO; fumonisin; mycotoxin; KW transgenic plant; detoxification; animal feed; silage; KW selectable marker; alpha mating factor; signal peptide; ss. XX OS Chimeric - Saccharomyces cerevisiae. OS Chimeric - Exophiala spinifera. XX | | | |

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FH Key Location/Qualifiers
FT CDS 1..1665
FT /tag= a
FT sig_peptide 1..267
FT /tag= b
FT /product= "yeast alpha mating factor secretion
FT signal"
FT mat_peptide 268..1662
FT /tag= c
FT /product= "K:trAPOA"
FT misc_feature 268..270
FT /tag= d
FT /note= "extra lysine"
XX
PN WO200004159-A1.
XX
XX 27-JAN-2000.
XX
XX 08-JUL-1999; 99WO-US15454.
XX
XX 15-JUL-1998; 98US-0092936.
XX 21-MAY-1999; 99US-0135391.
XX
XX (PION-) PIONEER HI-BRED INT INC.
XX (CURA-) CURAGEN CORP.
XX
XX Duvick JP, Gilliam JT, Maddox JR;
XX
XX WPI: 2000-182425/16.
XX P-PSDB: AAY58910.
XX
XX New isolated polynucleotides, polypeptides useful for detecting and
XX degrading fumonisin or structurally related mycotoxin in processed
XX grain or in silage.
XX
XX Example 8; Page 85-87; 154pp; English.
XX
XX The present sequence is that of polynucleotide pPic2alphaA:K:trAPOA
XX encoding a protein (see AAY58910) comprising the yeast alpha mating
XX factor signal peptide fused with K:trAPOA, a truncated, but
XX functional, amino polyol amine oxidase (APOA, see also AAY58909) of
XX Exophiala spinifera. The polynucleotide was designed for expression
XX in Pichia pastoris. The encoded protein is capable of degrading
XX fumonisin and related mycotoxins. The invention provides APOA
XX polynucleotides (see AAY58983-87) and polypeptides (see AAY58900-05) of
XX E. spinifera and Rhinocladiella atrovirens. The polynucleotides are
XX used to transform plant cells normally susceptible to Fusarium or
XX other toxin-producing fungus infection. Also provided are methods
XX for expressing APOA in transgenic plants, prokaryotic and non-plant
XX eukaryotic systems. Methods for detoxification of grain, grain
XX processing, silage, food crops and in animal feed and rumen
XX microorganisms are also disclosed. APOA polynucleotide can also be
XX used as a selectable marker.
XX
XX Sequence 1673 BP; 414 A; 430 C; 456 G; 373 T; 0 other;
XX
XX
XX Query Match 16.8%; Score 324; DB 21; Length 1673;
XX Best Local Similarity 99.7%; Pred. No. 1.8e-158;
XX Matches 374; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1555 CAATGGTCCATTACCTGTTTCATGTCGGAGACCCCGGACGGAAGTGGTCCCAACAGTCC 1614
XX |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX Db 1291 CAATGGTCCATTACCTGTTTCATGTCGGAGACCCCGGACGGAAGTGGTCCCAACAGTCC 1350
XX
XX QY 1615 AAGCAGGTACGACAAAGTCTGCTGGACCACTCCGCGCAGCTACGAGAACGCGGG 1674
XX |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX Db 1351 AAGCAGGTACGACAAAGTCTGCTGGACCACTCCGCGCAGCTACGAGAACGCGGG 1410
XX
XX QY 1675 GCCCAAGTCCCGAGCCGCCAACGTGCTCGAAATCGAGTGGTGGAGACGAGTATTC 1734
XX |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
XX Db 1411 GCCCAAGTCCCGAGCCGCCAACGTGCTCGAAATCGAGTGGTGGAGACGAGTATTC 1470
XX
XX QY 1735 CAAGGAGCTCCGAGCGCGCTCTATGGGCTGAACGATCTCATCAGTGGTTCGGCGCTC 1794
XX |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

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Db 1471 CAAGGAGCTCCGAGCGCGTCTATGGGCTGAACGATCTCATCAGTGGTTCGGCGCTC 1530
|||||
QY 1795 AGAAGCGCGTTCAAGTGTGTTCAATTTCGTTGGAACGAGACGTCCTTAGTTTGAAGGG 1854
|||||
Db 1531 AGAAGCGCGTTCAAGAGTGTTCATTTCTGTTGGAACGAGACGTCCTTAGTTTGAAGGG 1590
|||||
QY 1855 TATATGGAAGGGCCATACGATCGGTCACAGAGTCTGCAGAGTGTGTGGCTAGCCTG 1914
|||||
Db 1591 TATATGGAAGGGCCATACGATCGGTCACAGAGTCTGCAGAGTGTGTGGCTAGCCTG 1650
|||||
QY 1915 GTGCCAGCAGCATAG 1929
|||||
Db 1651 GTGCCAGCAGCATAG 1665
|||||

RESULT 12
AAZ60638
ID AAZ60638 standard; DNA; 1673 BP.
XX
XX AC AAZ60638;
XX
XX 16-MAY-2000 (first entry)
XX
XX DE DNA encoding an aminopolyol amine oxidase for expression in Pichia.
XX
XX KW Aminopolyol amine oxidase; APOA; mycotoxin degradation; antimicrobial;
XX plant fungal invasion; hydrogen peroxide; Fusarium; fungi; ss.
XX
XX OS Synthetic.
XX OS Exophiala spinifera.
XX
XX FH Key Location/Qualifiers
XX CDS 1..1665
XX /tag= a
XX /product= "aminopolyol amine oxidase"
XX sig_peptide 1..267
XX /tag= b
XX mat_peptide 268..1662
XX /tag= c
XX /note= "aminopolyol amine oxidase"
XX
XX WO200004160-A1.
XX
XX 27-JAN-2000.
XX
XX 08-JUL-1999; 99WO-US15455.
XX
XX 15-JUL-1998; 98US-0092936.
XX
XX (PION-) PIONEER HI-BRED INT INC.
XX (CURA-) CURAGEN CORP.
XX
XX Crasta OR, Duvick J, Folkerts O, Gilliam JT, Maddox JR;
XX
XX WPI: 2000-182426/16.
XX P-PSDB: AAY68846.
XX
XX New nucleic acid encoding aminopolyol amine oxidase, used, e.g. to
XX generate plants resistant to Fusarium.
XX
XX Example 8; Page 86-88; 145pp; English.
XX
XX The present sequence encodes a Exophiala spinifera aminopolyol amine
XX oxidase (APOA). The enzyme has homology to the flavin containing amine
XX oxidase family, that oxidise primary amine to an aldehyde or ketone,
XX releasing ammonia and hydrogen peroxide. The APOA enzyme degrades
XX mycotoxins that promote fungal invasion of plants. Destruction of
XX mycotoxins by APOA generates, as a by-product, hydrogen peroxide which
XX is itself an antimicrobial and stimulates the plants own defensive
XX systems. The APOA polynucleotides are used to generate plants
XX (particularly maize) that are resistant to Fusarium or other fungi

```

CC that produce mycotoxins and/or to degrade such mycotoxins (e.g. during
 CC ensiling); for recombinant production of APAO polypeptides; as
 CC selection markers for plant transformation; and to isolate related
 CC sequences from other organisms. The APAO polypeptides are used to
 CC degrade mycotoxins in plant materials, including expression in
 CC engineered bacteria and fungi, e.g. rumen microflora.

XX Sequence 1673 BP; 414 A; 430 C; 456 G; 373 T; 0 other;

Query Match 16.8%; Score 324; DB 21; Length 1673;
 Best Local Similarity 99.7%; Pred. No. 1.8e-158;
 Matches 374; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1555 CAATGGTCCATTACCTGTTTCATGTCGGAGACCGGGACGGAAGTGTGCCACAGTCC 1614
 DB 1291 CAATGGTCCATTACCTGTTTCATGTCGGAGACCGGGACGGAAGTGTGCCACAGTCC 1350
 QY 1615 AAGCAGGTACGACAAAAGTCTGTCTGGGACCAACTCCGGCAGCCTACGAGAACGCCGGG 1674
 DB 1351 AAGCAGGTACGACAAAAGTCTGTCTGGGACCAACTCCGGCAGCCTACGAGAACGCCGGG 1410
 QY 1675 GCCCAAGTCCAGAGCGCGCAACGCTCTGAAATCGAGTGTGGAAGCAGCAGTATTTC 1734
 DB 1411 GCCCAAGTCCAGAGCGCGCAACGCTCTGAAATCGAGTGTGGAAGCAGCAGTATTTC 1470
 QY 1735 CAAGGAGTCCGAGCGCGCTATATGGCTGAACGATCTCATCACACTGGTTCGGCGCTC 1794
 DB 1471 CAAGGAGTCCGAGCGCGCTATATGGCTGAACGATCTCATCACACTGGTTCGGCGCTC 1530
 QY 1795 AGAAGCGCGTTCAGAGTGTGTTTCATTTCTGGGAACGAGACGCTCTTTAGTTGGAAGGG 1854
 DB 1531 AGAAGCGCGTTCAGAGTGTGTTTCATTTCTGGGAACGAGACGCTCTTTAGTTGGAAGGG 1590
 QY 1855 TATATGGAAGGGCCATACGATCGGCTCAACGAGTGTCTGAGAGTGTCTGCTAGCCCTG 1914
 DB 1591 TATATGGAAGGGCCATACGATCGGCTCAACGAGTGTCTGAGAGTGTCTGCTAGCCCTG 1650
 QY 1915 GTGCCAGCAGCATAG 1929
 DB 1651 GTGCCAGCAGCATAG 1665

RESULT 13

AAZ58402
 ID AAZ58402 standard; cDNA; 1803 BP.

XX AC AAZ58402;

XX DT 23-MAY-2000 (first entry)

XX DE Exophiala spinifera amino polyol amine oxidase cDNA.

XX KW Amino polyol amine oxidase; fumonisin; mycotoxin; transgenic plant;
 KW detoxification; animal feed; silage; selectable marker; ds.

XX OS Exophiala spinifera.

XX PN WO200004159-A1.

XX PD 27-JAN-2000.

XX PF 08-JUL-1999; 99WO-US15454.

XX PR 15-JUL-1998; 98US-0092936.

XX PR 21-MAY-1999; 99US-0135391.

XX PA (PION-) PIONEER HI-BRED INT INC.

XX PA (CURA-) CURAGEN CORP.

XX PI Duvick JP, Gilliam JT, Maddox JR;

XX WPI; 2000-182425/16.

XX DR P-PSDB; AAY58913.

XX New isolated polynucleotides, polypeptides useful for detecting and
 PT degrading fumonisin or structurally related mycotoxin in processed
 PT grain or in silage
 XX Example 10; Page 97-100; 154pp; English.

XX The present sequence is that of the coding region of full-length
 CC amino polyol amine oxidase (APAO) cDNA of *Exophiala spinifera*
 CC 2141.10. APAO is capable of degrading fumonisin, its hydrolysis
 CC product API, and related mycotoxins. The invention provides APAO
 CC polynucleotides (see AAY58383-87) and polypeptides (see AAY58900-05) of
 CC *E. spinifera* and *Rhizoctonia* atrovirens. The polynucleotides are
 CC used to transform plant cells normally susceptible to *Fusarium* or
 CC other toxin-producing fungus infection. Transgenic plants can be
 CC regenerated from the transformed plant cells. Also provided are
 CC methods for expressing both APAO and a fumonisin-esterase in a
 CC transgenic plant, and for producing APAO enzyme in prokaryotic and
 CC non-plant eukaryotic systems. Transgenic plants capable of degrading
 CC fumonisin or of producing the degrading enzymes are provided.
 CC Methods for detoxification of grain, grain processing, silage, food
 CC crops and in animal feed and rumen microorganisms are also disclosed.
 CC APAO polynucleotide is also useful as a selectable marker.

XX Sequence 1803 BP; 424 A; 501 C; 502 G; 376 T; 0 other;

Query Match 16.8%; Score 324; DB 21; Length 1803;
 Best Local Similarity 99.7%; Pred. No. 1.8e-158;
 Matches 374; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1555 CAATGGTCCATTACCTGTTTCATGTCGGAGACCGGGACGGAAGTGTGCCACAGTCC 1614
 DB 1429 CAATGGTCCATTACCTGTTTCATGTCGGAGACCGGGACGGAAGTGTGCCACAGTCC 1488
 QY 1615 AAGCAGGTACGACAAAAGTCTGTCTGGGACCAACTCCGGCAGCCTACGAGAACGCCGGG 1674
 DB 1489 AAGCAGGTACGACAAAAGTCTGTCTGGGACCAACTCCGGCAGCCTACGAGAACGCCGGG 1548
 QY 1675 GCCCAAGTCCAGAGCGCGCAACGCTCTGAAATCGAGTGTGGAAGCAGCAGTATTTC 1734
 DB 1549 GCCCAAGTCCAGAGCGCGCAACGCTCTGAAATCGAGTGTGGAAGCAGCAGTATTTC 1608
 QY 1735 CAAGGAGTCCGAGCGCGCTATATGGCTGAACGATCTCATCACACTGGTTCGGCGCTC 1794
 DB 1609 CAAGGAGTCCGAGCGCGCTATATGGCTGAACGATCTCATCACACTGGTTCGGCGCTC 1668
 QY 1795 AGAAGCGCGTTCAGAGTGTGTTTCATTTCTGGGAACGAGACGCTCTTTAGTTGGAAGGG 1854
 DB 1669 AGAAGCGCGTTCAGAGTGTGTTTCATTTCTGGGAACGAGACGCTCTTTAGTTGGAAGGG 1728
 QY 1855 TATATGGAAGGGCCATACGATCGGCTCAACGAGTGTCTGAGAGTGTCTGCTAGCCCTG 1914
 DB 1729 TATATGGAAGGGCCATACGATCGGCTCAACGAGTGTCTGAGAGTGTCTGCTAGCCCTG 1788
 QY 1915 GTGCCAGCAGCATAG 1929
 DB 1789 GTGCCAGCAGCATAG 1803

RESULT 14

AAZ60641
 ID AAZ60641 standard; DNA; 1803 BP.

XX AC AAZ60641;

XX DT 16-MAY-2000 (first entry)

XX DE DNA encoding a full length aminopolyol amine oxidase APAO.

XX KW Aminopolyol amine oxidase; APAO; mycotoxin degradation; antimicrobial;
 KW plant fungal invasion; hydrogen peroxide; *Fusarium*; fungi; ss.
 XX OS *Exophiala spinifera*.

```
XX Key Location/Qualifiers
FH 1..1803
FT CDS
FT /*tag= a
FT /product= "aminopolylol amine oxidase"
XX
PN WO200004160-A1.
XX
XX 27-JAN-2000.
XX
XX 08-JUL-1999; 99WO-US15455.
XX
XX 15-JUL-1998; 98US-0092936.
XX
XX (PION-) PIONEER HI-BRED INT INC.
XX (CURA-) CURAGEN CORP.
XX
XX Crasta OR, Duvick J, Folkerts O, Gilliam JT, Maddox JR;
XX
XX WPI; 2000-182426/16.
XX P-PSDB; AAY68849.
XX
XX New nucleic acid encoding aminopolylol amine oxidase, used, e.g. to
XX generate plants resistant to Fusarium -
XX
XX Example 10; Page 99-101; 145pp; English.
XX
XX The present sequence encodes a full length Exophiala spinifera
XX aminopolylol amine oxidase (APAO). The enzyme has homology to the
XX flavin containing amine oxidase family, that oxidise primary amine
XX to an aldehyde or ketone, releasing ammonia and hydrogen peroxide.
XX The APAO enzyme degrades mycotoxins that promote fungal invasion of
XX plants. Destruction of mycotoxins by APAO generates, as a by-product,
XX hydrogen peroxide which is itself an antimicrobial and stimulates the
XX plants own defensive systems. The APAO polynucleotides are used to
XX generate plants (particularly maize) that are resistant to Fusarium or
XX other fungi that produce mycotoxins and/or to degrade such mycotoxins
XX (e.g. during ensilaging); for recombinant production of APAO
XX polypeptides; as selection markers for plant transformation; and to
XX isolate related sequences from other organisms. The APAO polypeptides
XX are used to degrade mycotoxins in plant materials, including expression
XX in engineered bacteria and fungi, e.g. rumen microflora.
XX
XX Sequence 1803 BP; 424 A; 501 C; 502 G; 376 T; 0 other;
XX
XX Query Match 16.8%; Score 324; DB 21; Length 1803;
XX Best Local Similarity 99.7%; Pred. No. 1.8e-158;
XX Matches 374; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1555 CAATGGTCCATTACCTGTTTCATGGTGGGAGACCGCGGACGGAAGTGGTCCCAACAGTCC 1614
XX |||||||
XX 1429 CAATGGTCCATTACCTGTTTCATGGTGGGAGACCGCGGACGGAAGTGGTCCCAACAGTCC 1488
XX |||||||
XX 1615 AGCAGGTACGACAAAGTCTGTCGGACCACTCCGGGAGCTACGAGAACGCCGGG 1674
XX |||||||
XX 1489 AGCAGGTACGACAAAGTCTGTCGGACCACTCCGGGAGCTACGAGAACGCCGGG 1548
XX |||||||
XX 1675 GCCCAAGTCCAGAGCCGCGCAACGTCGTAATCGAGTGGTGGAAACGACGATATTC 1734
XX |||||||
XX 1549 GCCCAAGTCCAGAGCCGCGCAACGTCGTAATCGAGTGGTGGAAACGACGATATTC 1608
XX |||||||
XX 1735 CAAGGAGTCCAGAGCGGCGTCTATGGGCTGAACGATCTCATCACTGGTTCGGCGCTC 1794
XX |||||||
XX 1609 CAAGGAGTCCAGAGCGGCGTCTATGGGCTGAACGATCTCATCACTGGTTCGGCGCTC 1668
XX |||||||
XX 1795 AGAAGCCGTTCAAGTGTGTTCAATTCGTTGGAGCGAGACGCTTTAGTTGGAAGGG 1854
XX |||||||
XX 1669 AGAAGCCGTTCAAGAGTGTTCATTTGTTGGAGCGAGACGCTTTAGTTGGAAGGG 1728
XX |||||||
XX 1855 TATATGGAAGGGGCGCATACGATCGGTCACACGAGTGTCTGCAAGAGTGTGGCTAGCGCTG 1914
XX |||||||
XX 1729 TATATGGAAGGGGCGCATACGATCGGTCACACGAGTGTCTGCAAGAGTGTGGCTAGCGCTG 1788
XX |||||||
```

```
Oy 1915 GTCCAGCAGCATAG 1929
|||||
Db 1789 GTCCAGCAGCATAG 1803

RESULT 15
AAZ58384
ID AAZ58384 standard; DNA; 1930 BP.
XX
XX AC AAZ58384;
XX
XX 23-MAY-2000 (first entry)
XX
XX Exophiala spinifera amino polyol amine oxidase ESP003_C12 DNA.
XX
XX Amino polyol amine oxidase; fumonisin; mycotoxin; transgenic plant;
XX detoxification; animal feed; silage; selectable marker; ds.
XX
XX Exophiala spinifera.
XX
XX Key Location/Qualifiers
FH 1..1930
FT CDS /*tag= a
FT /note= "contains introns"
FT intron 739..811
FT /*tag= b
FT intron 1134..1187
FT /*tag= c
XX
XX WO200004159-A1.
XX
XX 27-JAN-2000.
XX
XX 08-JUL-1999; 99WO-US15454.
XX
XX 15-JUL-1998; 98US-0092936.
XX 21-MAY-1999; 99US-0135391.
XX
XX (PION-) PIONEER HI-BRED INT INC.
XX (CURA-) CURAGEN CORP.
XX
XX Duvick JP, Gilliam JT, Maddox JR;
XX
XX WPI; 2000-182425/16.
XX P-PSDB; AAY58902.
XX
XX New isolated polynucleotides, polypeptides useful for detecting and
XX degrading fumonisins or structurally related mycotoxins in processed
XX grain or in silage ;
XX
XX Claim 1; Page 141-142; 154pp; English.
XX
XX The present sequence is that of an isolated nucleic acid,
XX designated ESP003_C12, of Exophiala spinifera isolate ESP002,
XX which encodes an amino polyol amine oxidase (APAO, see AAY58902)
XX capable of degrading fumonisins, its hydrolysis product API, and
XX related mycotoxins. The DNA was obtained by PCR amplification of
XX ESP003 mycellial DNA using primers based on APAO of E. spinifera
XX ATCC 74269. The invention provides APAO polynucleotides (see
XX AAZ58383-87) and polypeptides (see AAY58900-05) of E. spinifera and
XX Rhinocladiella atrovirens. The polynucleotides are used to transform
XX plant cells normally susceptible to Fusarium or other toxin-producing
XX fungus infection. Transgenic plants can be regenerated from the
XX transformed plant cells. Also provided are methods for expressing
XX both APAO and a fumonisin-esterase in a transgenic plant, and for
XX producing APAO enzyme in prokaryotic and non-plant eukaryotic
XX systems. Transgenic plants capable of degrading fumonisins or of
XX producing the degrading enzymes are provided. Methods for
XX detoxification of grain, grain processing, silage, food crops and
XX in animal feed and rumen microorganisms are also disclosed. APAO
XX polynucleotide is also useful as a selectable marker.
XX
XX Sequence 1930 BP; 449 A; 531 C; 537 G; 412 T; 1 other;
```

| | | | | | |
|-----------------------|--------------|--|--------------------|-----------|--------------|
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| Best Local Similarity | | 99.7%; | Pred No. 1.8e-158; | | |
| Matches 374; | Conservative | 0; | Mismatches 1; | Indels 0; | Gaps 0; |
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| Db | 1556 | CAATGGTCCATTACCTGTTTCATGGTCGGAGACCCGGGACCGAAGTGGTCCCAACAGTCC | 1615 | | |
| QY | 1615 | AAGCAGGTACGACAAAGTCTGTCTGGGACCAACTCCCGCAGCCTACGAGAACGCCGGG | 1674 | | |
| Db | 1616 | AAGCAGGTACGACAAAGTCTGTCTGGGACCAACTCCCGCAGCCTACGAGAACGCCGGG | 1675 | | |
| QY | 1675 | GCCCAAGTCCAGAGCGCGCCACGTCCTCGAAATCGAGTGGTCGAGCAGCAGTATTTC | 1734 | | |
| Db | 1676 | GCCCAAGTCCAGAGCGCGCCACGTCCTCGAAATCGAGTGGTCGAGCAGCAGTATTTC | 1735 | | |
| QY | 1735 | CAAGGAGCTCCGAGCGCCGCTATGGGCTGAACGATCTCATCACACTGGGTTGCGCGCTC | 1794 | | |
| Db | 1736 | CAAGGAGCTCCGAGCGCCGCTATGGGCTGAACGATCTCATCACACTGGGTTGCGCGCTC | 1795 | | |
| QY | 1795 | AGAACGCCGTTCAAGTGTTCATTTCGTTGGAACGGAGACGCTCTTTAGTTTGGAAAAGG | 1854 | | |
| Db | 1796 | AGAACGCCGTTCAAGTGTTCATTTCGTTGGAACGGAGACGCTCTTTAGTTTGGAAAAGG | 1855 | | |
| QY | 1855 | TATATGGAAGGGGCCATACGATCGGTCACGAGGTGCTGCAGAGTTGTGGCTAGCCTG | 1914 | | |
| Db | 1856 | TATATGGAAGGGGCCATACGATCGGTCACGAGGTGCTGCAGAGTTGTGGCTAGCCTG | 1915 | | |
| QY | 1915 | GTGCCAGCAGCATAG | 1929 | | |
| Db | 1916 | GTGCCAGCAGCATAG | 1930 | | |

Search completed: November 12, 2002, 05:41:50
Job time : 425 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 12, 2002, 04:43:45 ; Search time 2811 Seconds
(without alignments)
11113.872 Million cell updates/sec

Title: US-09-771-045A-35

Perfect score: 1929

Sequence: 1 atggcacttgccagcgacta.....gcctgggtgccagcagcatag 1929

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 16154066 seqs, 8097743376 residues

Word size : 0

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

EST.*

1: em_estba.*

2: em_esthum.*

3: em_estin.*

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6: em_estpi.*

7: em_estro.*

8: em_hic.*

9: gb_est1.*

10: gb_est2.*

11: gb_hic.*

12: gb_est3.*

13: gb_est4.*

14: gb_est5.*

15: em_estfun.*

16: em_estom.*

17: gb_gss.*

18: em_gss_hum.*

19: em_gss_inv.*

20: em_gss_pln.*

21: em_gss_vrt.*

22: em_gss_fun.*

23: em_gss_mam.*

24: em_gss_mus.*

25: em_gss_other.*

26: em_gss_pro.*

27: em_gss_rod.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------------|--------------------|
| 1 | 23 | 1.2 | 623 | 17 AQ280543 | AQ280543 CITBI-E1- |
| C 2 | 21 | 1.1 | 1284 | 14 BM803905 | BM803905 AGENCOURT |
| C 3 | 20 | 1.0 | 285 | 13 BI050480 | BI050480 CM3-GN031 |
| C 4 | 20 | 1.0 | 434 | 17 AQ046343 | AQ046343 RPI111-34 |
| C 5 | 20 | 1.0 | 526 | 17 AQ697937 | AQ697937 HS_5536_B |
| C 6 | 20 | 1.0 | 716 | 9 AUI33639 | AUI33639 AUI33639 |

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| 7 | 20 | 1.0 | 807 | 12 BG522272 | BG522272 2-42 Stev |
| C 8 | 20 | 1.0 | 922 | 17 AG059979 | AG059979 Pan trogl |
| 9 | 19 | 1.0 | 80 | 17 BH811443 | BH811443 SALK_0586 |
| 10 | 19 | 1.0 | 119 | 10 AW783945 | AW783945 P2T1L6 PL |
| C 11 | 19 | 1.0 | 181 | 9 AL710341 | AL710341 DKZp866H |
| C 12 | 19 | 1.0 | 182 | 10 BE560457 | BE560457 601346723 |
| C 13 | 19 | 1.0 | 184 | 14 BQ805991 | BQ805991 WHE3573_E |
| C 14 | 19 | 1.0 | 185 | 10 BE264866 | BE264866 601194354 |
| C 15 | 19 | 1.0 | 201 | 12 BE796178 | BE796178 601591321 |
| C 16 | 19 | 1.0 | 212 | 12 BE714854 | BE714854 IL5-HT073 |
| C 17 | 19 | 1.0 | 213 | 12 BE903091 | BE903091 601677147 |
| C 18 | 19 | 1.0 | 218 | 12 BF204571 | BF204571 601868184 |
| C 19 | 19 | 1.0 | 223 | 12 BE714855 | BE714855 IL5-HT073 |
| C 20 | 19 | 1.0 | 225 | 12 BG386968 | BG386968 602455159 |
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| C 22 | 19 | 1.0 | 227 | 12 BG386339 | BG386339 602455540 |
| C 23 | 19 | 1.0 | 227 | 13 BI200064 | BI200064 602760735 |
| C 24 | 19 | 1.0 | 233 | 10 BE249908 | BE249908 600942953 |
| C 25 | 19 | 1.0 | 234 | 10 BE267669 | BE267669 601124928 |
| C 26 | 19 | 1.0 | 236 | 10 BE267625 | BE267625 601124848 |
| C 27 | 19 | 1.0 | 240 | 12 BF308488 | BF308488 601887626 |
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| C 29 | 19 | 1.0 | 242 | 12 BE899487 | BE899487 601682278 |
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| C 41 | 19 | 1.0 | 373 | 9 AA542887 | AA542887 ni98a02.s |
| C 42 | 19 | 1.0 | 373 | 13 BI005958 | BI005958 CM2-RT006 |
| C 43 | 19 | 1.0 | 390 | 14 BM755698 | BM755698 K-EST0033 |
| C 44 | 19 | 1.0 | 392 | 9 AI450161 | AI450161 mt86d08.X |
| C 45 | 19 | 1.0 | 406 | 10 AW504032 | AW504032 UI-HF-BNO |

ALIGNMENTS

| | | | | | |
|------------|--|------------|--------------|---------------|-----------------|
| RESULT 1 | AQ280543 | 623 bp | DNA | linear | GSS 22-NOV-1998 |
| LOCUS | CITBI-E1-251406.TF | CITBI-E1 | Homo sapiens | genomic clone | 251406, DNA |
| DEFINITION | sequence. | | | | |
| ACCESSION | AQ280543 | | | | |
| VERSION | AQ280543.1 | GI:3906362 | | | |
| KEYWORDS | GSS. | | | | |
| SOURCE | human. | | | | |
| ORGANISM | Homo sapiens | | | | |
| REFERENCE | 1 (bases 1 to 623) | | | | |
| AUTHORS | Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linber, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C. | | | | |
| TITLE | Use of a random human BAC End Sequence Database for Sequence-Ready Map Building | | | | |
| JOURNAL | Unpublished (1998) | | | | |
| COMMENT | Other GSSs: CITBI-E1-251406.TR | | | | |
| | Contact: Mark Adams | | | | |
| | Department of Eukaryotic Genomics | | | | |
| | The Institute for Genomic Research | | | | |
| | 9712 Medical Center Dr., Rockville, MD 20850, USA | | | | |
| | Tel: 301 838 0200 | | | | |
| | Fax: 301 838 0208 | | | | |
| | Email: mdamads@tigr.org | | | | |
| | Clones are available from Research Genetics (info@resgen.com). BAC | | | | |
| | end search page: | | | | |

http://www.tigr.org/tdb/hungen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.

FEATURES

source

Location/Qualifiers
1. .623
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="251406"
/clone_lib="CITBI-El"
/sex="male"
/cell_type="sperm"
/note="Vector: pBelOAC11; Site_1: EcoRI; Site_2: EcoRI;
Caltech Human BAC Library D"

BASE COUNT 136 a 192 c 94 g 200 t 1 others
ORIGIN

Query Match 1.2%; Score 23; DB 17; Length 623;
Best Local Similarity 100.0%; Pred. No. 0.81; Mismatches 0; Indels 0; Gaps 0;
Matches 23; Conservative 0;

Qy 783 AATACAGTCACTGACTCCACTTC 805
|||||
Db 139 AATACAGTCACTGACTCCACTTC 161

RESULT-2

BM803905/c

LOCUS

DEFINITION BM803905 1284 bp mRNA linear EST 05-MAR-2002
AGENCOURT_6439488 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5520605

5', mRNA sequence.

ACCESSION

BM803905

VERSION

BM803905.1

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 1284)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgaabs@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing By: The I.M.A.G.E. Consortium (LLNL)

Clone Distribution: Agencourt Bioscience Corporation

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM12184 row: o column: 06

High quality sequence stop: 453.

Location/Qualifiers

1. .1284

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:5520605"

/clone_lib="NIH_MGC_71"

/tissue_type="leiomyosarcoma"

/lab_host="DH10B (phage-resistant)"

/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI;

Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 2.1 kb.

BASE COUNT 260 a 382 g 362 t 276 c 4 others

ORIGIN

Query Match

Best Local Similarity 1.1%; Score 21; DB 14; Length 1284;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 429 CGTGGTAGTGGCGCTGG 449

Db 1196 CGTGGTAGTGGCGCTGG 1176

RESULT 3

BI050480/c

LOCUS

DEFINITION

CM3-CN0313-050101-593-e06 GN0313 Homo sapiens cDNA, mRNA sequence.

ACCESSION

BI050480

VERSION

BI050480.1

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 285)

Dias Neto, E., Garcia Correa, R., Verjovsky-Almeida, S., Briones, M.R.,

Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,

Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,

Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare

, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and

Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL

{http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM3&t2=CM3-GN0313-

050101-593-e06&t3=2001-01-05&t4=1}

Seq primer: puc 18 forward

High quality sequence start: 8

High quality sequence stop: 285.

Location/Qualifiers

1. .285

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone_lib="GN0313"

/dev_stage="Adult"

/note="Organ: placenta_normal; Vector: puc18; Site_1: SmaI

; Site_2: SmaI; A mini-library was made by cloning

products derived from ORSTES PCR (U.S. Letters Patent

application No. 196,716 - Ludwig Institute for Cancer

Research) profiles into the puc 18 vector. Reverse

transcription of tissue mRNA and cDNA amplification were

performed under low stringency conditions."

BASE COUNT 73 a 70 c 53 g 89 t

ORIGIN

Query Match

Best Local Similarity 1.0%; Score 20; DB 13; Length 285;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1625 GACAAAGTCTGCTGGGAC 1644

Db 173 GACAAAGTCTGCTGGGAC 154

RESULT 4

AQ046343/c

LOCUS

DEFINITION

RPC111-34118.TK RPCI-11 Homo sapiens genomic clone RPCI-11-34118,

DNA sequence.

ACCESSION

AQ046343

VERSION

AQ046343.1

KEYWORDS

GSS.

SOURCE

human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 434)
AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C.
TITLE Use of BAC End Sequences for Sequence-Ready Map Building (1998)
JOURNAL Unpublished (1998)
COMMENT Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tldb/humgen/bac_end_search/bac_end_search.html
Class: BAC ends.

FEATURES Source
1..434
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="RPCI-11-34118"
/clone_lib="RPCI-11"
/sex="Male"
/cell_type="Lymphocytes"
/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI; RPC111 Human Male BAC Library"

BASE COUNT 119 a 90 c 80 g 145 t
ORIGIN

Query Match 1.0%; Score 20; DB 17; Length 434;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1176 GGTCAATCCAGTATGCAGT 1195
|||||
Db 190 GGTCAATCCAGTATGCAGT 171

RESULT 5
LOCUS AQ697937 526 bp DNA linear GSS 06-JUL-1999
DEFINITION HS_3536_B1_G09_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate-1112 Col-17 Row-N, DNA sequence.
ACCESSION AQ697937
VERSION AQ697937.1 GI:5388185
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 526)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 434)
AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C.
TITLE Use of BAC End Sequences for Sequence-Ready Map Building (1998)
JOURNAL Unpublished (1998)
COMMENT Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tldb/humgen/bac_end_search/bac_end_search.html
Class: BAC ends.

FEATURES Source
1..526
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate-1112 Col=17 Row=N"
/clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBAC3.6 vector at EcoRI sites"

BASE COUNT 159 a 104 c 76 g 185 t
ORIGIN

Query Match 1.0%; Score 20; DB 17; Length 526;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1358 ATCCACCTTGACATTTC 1377
|||||
Db 403 ATCCACCTTGACATTTC 422

RESULT 6
LOCUS AU133639/c 716 bp mRNA linear EST 01-AUG-2002
DEFINITION AU133639 OVARC1 Homo sapiens cDNA clone OVARC1000332 5', mRNA sequence.
ACCESSION AU133639
VERSION AU133639.1 GI:10994178
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 716)
AUTHORS Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and Isogai,T.
TITLE HRI human cDNA project
JOURNAL Unpublished (2000)
COMMENT Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.
LOCATION/Qualifiers
1..716
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="OVARC1000332"
/clone_lib="OVARC1"
/tissue.type="ovary, tumor tissue"
/note="Vector: pME18SFL3"

BASE COUNT 168 a 197 c 193 g 155 t
ORIGIN

Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering.bac.htm) or from Research Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu
Plate: 1112 row: N column: 17
Seq primer: SP6
Class: BAC ends
High quality sequence stop: 526.
LOCATION/Qualifiers
1..526
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate-1112 Col=17 Row=N"
/clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBAC3.6 vector at EcoRI sites"

BASE COUNT 159 a 104 c 76 g 185 t
ORIGIN

Query Match 1.0%; Score 20; DB 17; Length 526;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1358 ATCCACCTTGACATTTC 1377
|||||
Db 403 ATCCACCTTGACATTTC 422

RESULT 6
LOCUS AU133639/c 716 bp mRNA linear EST 01-AUG-2002
DEFINITION AU133639 OVARC1 Homo sapiens cDNA clone OVARC1000332 5', mRNA sequence.
ACCESSION AU133639
VERSION AU133639.1 GI:10994178
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 716)
AUTHORS Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and Isogai,T.
TITLE HRI human cDNA project
JOURNAL Unpublished (2000)
COMMENT Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.
LOCATION/Qualifiers
1..716
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="OVARC1000332"
/clone_lib="OVARC1"
/tissue.type="ovary, tumor tissue"
/note="Vector: pME18SFL3"

BASE COUNT 168 a 197 c 193 g 155 t
ORIGIN

```

Query Match      1.0%; Score 20; DB 9; Length 716;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1667 ACGCCGGGCGCCCAAGTCCCA 1686
DB 79 ACGCCGGGCGCCCAAGTCCCA 60

RESULT 7
LOCUS      BG522272      807 bp mRNA linear EST 01-FEB-2002
DEFINITION 2-42 Stevia field grown leaf cDNA Stevia rebaudiana cDNA 5', mRNA
ACCESSION  BG522272
VERSION     BG522272.1 GI:18465336
KEYWORDS   EST.
SOURCE     Stevia rebaudiana.
ORGANISM   Stevia rebaudiana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Asterales; Asteraceae; Asteroideae;
Heliantheae; Stevia.
1 (bases 1 to 807)
REFERENCE
AUTHORS    Brande, J.E., Richman, A., Swanson, A.K. and Chapman, B.P.
TITLE      Leaf ESTs from Stevia rebaudiana: A resource for gene discovery in
JOURNAL    diterpene synthesis
COMMENT    Unpublished (2001)
CONTACT:   Jim Brande
Genomics and Biotechnology
Agriculture and Agri-Food Canada - SCPPRC
1391 Sandford St., London, Ontario, CANADA, N5V 4T3
Tel: 519 457 1470
Fax: 519 457 3997
Email: brandeje@em.agr.ca
Seq primer: T3 promoter primer.
FEATURES             source
     1..807
     /organism="Stevia rebaudiana"
     /strain="751/1501"
     /cultivar="Landrace"
     /db_xref="taxon:55670"
     /clone_lib="Stevia field grown leaf cDNA"
     /dev_stage="field grown, mid-size"
     /tissue_type="leaf"
     /note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI; This
cDNA library was constructed from polyA+ enriched mRNA
from field grown leaves. Mid-size actively growing leaves
were collected and pooled from several plants and frozen
immediately after harvesting in liquid nitrogen. The cDNA
was prepared using an XhoI-poly(dT) linker-primer. An
EcoRI adapter was ligated to the blunt end cDNA and the
products were digested with EcoRI and XhoI enabling
directional cloning into the lambda ZAP Express vector.
The library was amplified using the host strain XL1-Blue
MR'. Mass excision of the library was performed to
obtain pBK-CMV phagemid clones in the host strain XL0LR.
Single pass DNA sequencing was performed using the T3
promoter primer: 5' ATTACCTTCACTAAGGGA 3'. This library
was constructed by Alex Richman."
BASE COUNT      245 a 144 c 179 g 232 t 7 others
ORIGIN

Query Match      1.0%; Score 20; DB 12; Length 807;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 821 GAGTTTGCAGTGCAGTTCG 840
DB 355 GAGTTTGCAGTGCAGTTCG 374

RESULT 8
LOCUS      AG059979/c      922 bp DNA linear GSS 03-NOV-2001
DEFINITION Pan troglodytes DNA, clone: PTB-047F09.R, genomic survey sequence.
ACCESSION  AG059979
VERSION     AG059979.1 GI:16611209
KEYWORDS   GSS.
SOURCE     Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
ORGANISM   Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of Library PTB
Unpublished
2 (bases 1 to 922)
REFERENCE
AUTHORS    Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
TITLE      Direct Submission
JOURNAL    Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Sueniro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
[E-mail:chimpsesgsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170]
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
clone tracking errors.
PRIMERS
Sequencing: M13Rev
LIBRARY
Vector      : pKS145
R.Site 1    : SacI
R.Site 2    : SacI.
FEATURES             source
     1..922
     /organism="Pan troglodytes"
     /db_xref="taxon:9598"
     /clone="PTB-047F09.R"
     /sex="male"
     /cell_type="lymphoblast"
     /clone_lib="PTB Chimpanzee Male BAC Library"
BASE COUNT      51 a 271 c 355 g 243 t 2 others
ORIGIN

Query Match      1.0%; Score 20; DB 17; Length 922;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 CCACATCGCGGTAGGCCCA 78
DB 740 CCACATCGCGGTAGGCCCA 721

RESULT 9
LOCUS      BH811443      80 bp DNA linear GSS 02-MAY-2002
DEFINITION SALK_058617 Arabidopsis thaliana TDNA insertion lines Arabidopsis
thaliana genomic clone SALK_058617, DNA sequence.
ACCESSION  BH811443
VERSION     BH811443.1 GI:20389898
KEYWORDS   GSS.
SOURCE     thale cress.
ORGANISM   Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 80)
REFERENCE
AUTHORS    Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab
, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P.
, Zimmerman, J. and Ecker, J.R.

```

TITLE A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu

This is single pass sequence recovered from the left border of TDNA. This sequence lies within an annotated exon of Atlg47210 and an annotated exon of Atlg47210.
Class: TDNA tagged.

FEATURES Location/Qualifiers

1..80

/organism="Arabidopsis thaliana"

/strain="Columbia 0"

/db_xref="taxon:3702"

/clone="SALK_058617"

/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

BASE COUNT 14 a 22 c 15 g 29 t
ORIGIN

Query Match 1.0%; Score 19; DB 17; Length 80;

Best Local Similarity 100.0%; Pred. No. 82;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 346 GCCTTGGCTTACCTGAAT 364

|||||

Db 61 GCCTTGGCTTACCTGAAT 79

RESULT 10

AW783945

LOCUS

DEFINITION P21116 Plasmodium yoelii infected liver tissues EST 22-NOV-2000

Similar to liver and blood stage P. yoelii antigen, mRNA sequence.

ACCESSION AW783945.1 GI:7838321

VERSION

KEYWORDS

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 119)

Laurel, J., Sacci, J.B. Jr and Azad, A.F.

Retrieving parasite specific liver stage gene products in

Plasmodium yoelii infected livers using differential display

Mol. Biochem. Parasitol. 111, 143-151 (2000)

20542037

COMMENT

Contact: Lau, AOT

Dept. of Microbiology and Immunology

University of Maryland, Baltimore

655 W. Baltimore Street, BRB 3-034, Baltimore, MD 21201, USA

Tel: 410-706-7066

Fax: 410-706-0282

Email: alau@umaryland.edu

PCR Primers

FORWARD: TGTATACCTGATTAC

BACKWARD: CTACAGTGGCTTAATAC

Insert Length: 119 Std Error: 0.00.

Location/Qualifiers

1..119

/organism="Mus musculus"

/strain="BALB/c"

/db_xref="taxon:10090"

/clone_lib="Plasmodium yoelii infected liver tissues"
/tissue_type="liver"
/note="Organ: liver; P. yoelii sporozoites were IV injected into BALB/c mice and livers were harvested 24 hours post injection. Total RNA was processed and differential display was performed on the infected liver samples along with uninfected BALB/c liver control."
BASE COUNT 31 a 16 c 19 g 53 t
ORIGIN

Query Match 1.0%; Score 19; DB 10; Length 119;

Best Local Similarity 100.0%; Pred. No. 89;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1803 GTTCAAGTGTCTTCATTC 1821

|||||

Db 43 GTTCAAGTGTCTTCATTC 61

RESULT 11

AL710341/c

LOCUS

DEFINITION DKFZp686H1969_r1 686 (synonym: hlcc3) Homo sapiens CDNA clone

DKFZp686H1969 5', mRNA sequence.

ACCESSION AL710341

VERSION

KEYWORDS

EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 181)

Ansorge, W., Wirkner, U., Mewes, H.W., Weil, B. and Wiemann, S.

EST (Ansorge, W., Wirkner, U., Mewes, H.W., Weil, B. and Wiemann, S.)

Unpublished (1999)

CONTACT: Ansorge W

MIPS

Am Klopferspitz 18a D-82152 Martinsried, Germany

This is the 5' sequence of the clone insert

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer

Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;

sequenced by EMBL (European Molecular Biology Laboratories,

Heidelberg/Germany) within the CDNA sequencing consortium of the

German Genome Project.

No si sequence available.

This clone (DKFZp686H1969) is available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES

Location/Qualifiers

1..181

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="DKFZp686H1969"

/clone_lib="686 (synonym: hlcc3)"

/tissue_type="human skeletal muscle"

/dev_host="adult"

/lab_host="DH10B"

/note="vector: pTriplex2; Site_1: SfiI; Site_2: SfiIb;

CDNA-collection"

BASE COUNT 26 a 57 c 64 g 31 t 3 others

ORIGIN

Query Match 1.0%; Score 19; DB 9; Length 181;

Best Local Similarity 100.0%; Pred. No. 98;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1668 CGCCGGGGCCCAAGTCCCA 1685

|||||

Db 66 CGCCGGGGCCCAAGTCCCA 48

RESULT 12

BE560457/c

LOCUS BE560457 182 bp mRNA linear EST 15-AUG-2000
 DEFINITION 601346723f1 NIH_MGC_8 Homo sapiens cDNA clone IMAGE:3687725 5',
 mRNA sequence.
 ACCESSION BE560457
 VERSION BE560457.1 GI:9804177
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 182)
 AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-r@mail.nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
 Plate: LICM379 row: m column: 06
 High quality sequence start: 3
 High quality sequence stop: 182.
 Location/Qualifiers
 1..182
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:3687725"
 /clone_1ib="NIH_MGC_8"
 /tissue_type="Burkitt lymphoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: lymph; Vector: pORF7; Site_1: XhoI; Site_2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCACGAG(G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."
 26 a 65 c 31 t
 BASE COUNT
 ORIGIN
 Query Match 1.0%; Score 19; DB 10; Length 182;
 Best Local Similarity 100.0%; Pred. No. 98;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1668 CGCCGGGGCCCAAGTCCCA 1686
 |||||
 Db 34 CGCCGGGGCCCAAGTCCCA 16
 RESULT 13
 BQ805991 184 bp mRNA linear EST 31-JUL-2002
 LOCUS WHE35733_E02_J03S2 wheat developing grains cDNA library Triticum
 DEFINITION aestivum cDNA clone WHE35733_E02_J03, mRNA sequence.
 ACCESSION BQ805991
 VERSION BQ805991.1 GI:22030200
 KEYWORDS EST.
 SOURCE bread wheat.
 ORGANISM Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
 ; Triticeae; Triticum.
 1 (bases 1 to 184)
 Altenbach, S., Anderson, O.D., Chao, S., Chin, A., Close, T.J., Cronin
 K., Crossman, C., Fenton, R.D., Lazo, G.R., Pham, J., Rausch, C.J.,
 Wilson, C. and Woo, J.
 TITLE The structure and function of the expressed portion of the wheat
 genomes - Developing grains cDNA library
 JOURNAL Unpublished (2002)

COMMENT Contact: Olin Anderson
 US Department of Agriculture, Agriculture Research Service, Pacific
 West Area, Western Regional Research Center
 800 Buchanan Street, Albany, CA 94710, USA
 Tel: 5105595773
 Fax: 5105595818
 Email: anderson@pw.usda.gov
 Sequences have been trimmed to remove vector sequence and low
 quality sequence with phred score less than 20
 Seq primer: SK primer.
 FEATURES
 source
 1..184
 /organism="Triticum aestivum"
 /cultivar="Butte 86"
 /db_xref="taxon:4565"
 /clone="WHE35733_E02_J03"
 /clone_lib="Wheat developing grains cDNA library"
 /tissue_type="whole grains"
 /dev_stage="3-44 days post anthesis seed"
 /lab_host="E. coli SOLR"
 /note="Vector: Lambda ZAP II, excised phagemid; Site_1:
 EcoRI; Plants were grown under six following different
 environmental regimes in greenhouse. Environment 1)
 240C/170C day/night, well-watered, with post-anthesis
 fertilizer, Environment 2) 240C/170C day/night,
 well-watered, without post-anthesis fertilizer,
 Environment 3) 370C/170C day/night, well-watered, with
 post-anthesis fertilizer, Environment 4) 370C/170C
 day/night, well-watered, without post-anthesis fertilizer,
 Environment 5) 370C/170C day/night plus drought, with
 post-anthesis fertilizer, Environment 6) 370C/170C
 day/night plus drought, without post-anthesis fertilizer,
 developing wheat grains from the following were excised
 and frozen in liquid nitrogen, Environment 1 at 3, 5, 7,
 8, 10, 12, 16, 20, 24, 28, 32, 36, 40, 44 DPA Environment
 2 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 32, 36, 40, 44
 DPA Environment 3 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28,
 32, 34 DPA Environment 4 at 3, 5, 7, 8, 10, 12, 16, 20, 24,
 28, 32, 34 DPA Environment 5 at 3, 5, 7, 8, 10, 12, 16,
 20, 24, 28, 30 DPA Environment 6 at 3, 5, 7, 8, 10, 12, 16,
 20, 24, 28, 30 DPA and total RNA was prepared by S.
 Altenbach and K. Cronin at USDA-ARS, Albany, CA. A cDNA
 library was made using poly (A) RNA, and the cDNA clones
 were in vivo excised to give pBluescript SK(-) phagemids
 in the TJ Close lab (Chin, Close, Fenton) at the
 University of California, Riverside. Plasmid DNA
 preparations and DNA sequencing were performed in the OD
 Anderson lab (others)."
 32 a 47 c 49 g 56 t
 BASE COUNT
 ORIGIN
 Query Match 1.0%; Score 19; DB 14; Length 184;
 Best Local Similarity 100.0%; Pred. No. 98;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 187 GCTTGCCTTCTGCAGTTG 205
 |||||
 Db 108 GCTTGCCTTCTGCAGTTG 126
 RESULT 14
 BE264866/c 185 bp mRNA linear EST 13-JUL-2000
 LOCUS 601194354f1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3538309 5',
 mRNA sequence.
 ACCESSION BE264866
 VERSION BE264866.1 GI:9138427
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 185)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Plate: LLCM223 row: k column: 14
High quality sequence start: 4
High quality sequence stop: 185.
Location/Qualifiers
FEATURES
source
1..185
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3538309"
/clone_lib="NIH_MGC_7"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT 26 a 64 c 61 g 34 t
ORIGIN
Query Match 1.0%; Score 19; DB 10; Length 185;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1668 CGCCGGGGCCCAAGTCCCA 1686
|||||
Db 37 CGCCGGGGCCCAAGTCCCA 19
RESULT 15
BE796178/c
LOCUS BE796178 201 bp mRNA linear EST 20-SEP-2000
DEFINITION 601591321F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3945316 5',
mRNA sequence.
ACCESSION BE796178
VERSION BE796178.1 GI:10217376
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 201)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/PTP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM803 row: j column: 05
High quality sequence stop: 201.
Location/Qualifiers
FEATURES
source
1..201
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3945316"
/clone_lib="NIH_MGC_7"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:

EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT 27 a 72 c 66 g 36 t
ORIGIN
Query Match 1.0%; Score 19; DB 12; Length 201;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1668 CGCCGGGGCCCAAGTCCCA 1686
|||||
Db 53 CGCCGGGGCCCAAGTCCCA 35
Search completed: November 12, 2002, 06:28:56
Job time : 2820 secs



| | 7 | 20 | 1.0 | 807 | 12 | BG522272 | 2-42 Stev |
|--|---|----|-----|-----|----|----------|-----------|
| GenCore version 5.1.3 | | | | | | | |
| Copyright (c) 1993 - 2002 CompuGen Ltd. | | | | | | | |
| OM nucleic - nucleic search, using sw model | | | | | | | |
| Run on: November 12, 2002, 04:43:45 ; Search time 2811 Seconds | | | | | | | |
| (without alignments) | | | | | | | |
| 11113.872 Million cell updates/sec | | | | | | | |
| Title: US-09-771-045A-35 | | | | | | | |
| Perfect score: 1929 | | | | | | | |
| Sequence: 1 atggcacttcacgcagcta.....gcctggcgccagcagcatag 1929 | | | | | | | |
| Scoring table: OLIGO_NUC | | | | | | | |
| Gapop 60.0 , Gapext 60.0 | | | | | | | |
| Searched: 16154066 seqs, 8097743376 residues | | | | | | | |
| Word size : 0 | | | | | | | |
| Total number of hits satisfying chosen parameters: 32308132 | | | | | | | |
| Minimum DB seq length: 0 | | | | | | | |
| Maximum DB seq length: 2000000000 | | | | | | | |
| Post-processing: Listing first 45 summaries | | | | | | | |
| Database : | | | | | | | |
| EST:* | | | | | | | |
| 1: em_estba:* | | | | | | | |
| 2: em_esthum:* | | | | | | | |
| 3: em_estin:* | | | | | | | |
| 4: em_estmu:* | | | | | | | |
| 5: em_estov:* | | | | | | | |
| 6: em_estpl:* | | | | | | | |
| 7: em_estro:* | | | | | | | |
| 8: em_htc:* | | | | | | | |
| 9: qb_estl:* | | | | | | | |

ALIGNMENTS

```

RESULT 1
AQ280543
AQ280543
LOCUS
DEFINITION
    AQ280543 623 bp DNA linear GSS 22-NOV-1998
    CITBI-EL-251406.TF CITBI-EL Homo sapiens genomic clone 251406, DNA
    sequence.
ACCESSION
    AQ280543
VERSION
    AQ280543.1 GI:3906362
KEYWORDS
    GSS.
SOURCE
    human.
ORGANISM
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 623)
ADAMS,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,
ADAMS,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,
BERRY,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and
Venter,J.C.
Use of a random human BAC End Sequence Database for Sequence-Ready
Map Building
Unpublished (1998)
Other_GSSs: CITBI-EL-251406.TR
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 23 | 1.2 | 623 | 17 | AQ2803543 |
| c | 2 | 1.1 | 1284 | 14 | BM803905 |
| c | 3 | 2.0 | 285 | 13 | BI050480 |
| c | 4 | 2.0 | 434 | 17 | AQ046343 |
| c | 5 | 2.0 | 526 | 17 | AQ697937 |
| c | 6 | 2.0 | 716 | 9 | AU133639 |
| c | 7 | 2.0 | 716 | 9 | AU133639 |
| c | 8 | 2.0 | 716 | 9 | AU133639 |
| c | 9 | 2.0 | 716 | 9 | AU133639 |
| c | 10 | 2.0 | 716 | 9 | AU133639 |
| c | 11 | 2.0 | 716 | 9 | AU133639 |
| c | 12 | 2.0 | 716 | 9 | AU133639 |
| c | 13 | 2.0 | 716 | 9 | AU133639 |
| c | 14 | 2.0 | 716 | 9 | AU133639 |
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| c | 16 | 2.0 | 716 | 9 | AU133639 |
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| c | 19 | 2.0 | 716 | 9 | AU133639 |
| c | 20 | 2.0 | 716 | 9 | AU133639 |
| c | 21 | 2.0 | 716 | 9 | AU133639 |
| c | 22 | 2.0 | 716 | 9 | AU133639 |
| c | 23 | 2.0 | 716 | 9 | AU133639 |
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| c | 25 | 2.0 | 716 | 9 | AU133639 |
| c | 26 | 2.0 | 716 | 9 | AU133639 |
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| c | 28 | 2.0 | 716 | 9 | AU133639 |
| c | 29 | 2.0 | 716 | 9 | AU133639 |
| c | 30 | 2.0 | 716 | 9 | AU133639 |
| c | 31 | 2.0 | 716 | 9 | AU133639 |
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| c | 73 | 2.0 | 716 | 9 | AU133639 |
| c | 74 | 2.0 | 716 | 9 | AU133639 |
| c | 75 | 2.0 | 716 | 9 | AU133639 |
| c | 76 | 2.0 | 716 | 9 | AU133639 |
| c | 77 | 2.0 | 716 | 9 | AU133639 |
| c | 78 | 2.0 | 716 | 9 | AU133639 |
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| c | 88 | 2.0 | 716 | 9 | AU133639 |
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| c | 90 | 2.0 | 716 | 9 | AU133639 |
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| c | 92 | 2.0 | 716 | 9 | AU133639 |
| c | 93 | 2.0 | 716 | 9 | AU133639 |
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| c | 95 | 2.0 | 716 | 9 | AU133639 |
| c | 96 | 2.0 | 716 | 9 | AU133639 |
| c | 97 | 2.0 | 716 | 9 | AU133639 |
| c | 98 | 2.0 | 716 | 9 | AU133639 |
| c | 99 | 2.0 | 716 | 9 | AU133639 |
| c | 100 | 2.0 | 716 | 9 | AU133639 |
| c | 101 | 2.0 | 716 | 9 | AU133639 |
| c | 102 | 2.0 | 716 | 9 | AU133639 |
| c | 103 | 2.0 | 716 | 9 | AU133639 |
| c | 104 | 2.0 | 716 | 9 | AU133639 |
| c | 105 | 2.0 | 716 | 9 | AU133639 |
| c | 106 | 2.0 | 716 | 9 | AU133639 |
| c | 107 | 2.0 | 716 | 9 | AU133639 |
| c | 108 | 2.0 | 716 | 9 | AU133639 |
| c | 109 | 2.0 | 716 | 9 | AU133639 |
| c | 110 | 2.0 | 716 | 9 | AU133639 |
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| c | 113 | 2.0 | 716 | 9 | AU133639 |
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| c | 115 | 2.0 | 716 | 9 | AU133639 |
| c | 116 | 2.0 | 716 | 9 | AU133639 |
| c | 117 | 2.0 | 716 | 9 | AU133639 |
| c | 118 | 2.0 | 716 | 9 | AU133639 |
| c | 119 | 2.0 | 716 | 9 | AU133639 |
| c | 120 | 2.0 | 716 | 9 | AU133639 |
| c | 121 | 2.0 | 716 | 9 | AU133639 |
| c | 122 | 2.0 | 716 | 9 | AU133639 |
| c | 123 | 2.0 | 716 | 9 | AU133639 |
| c | 124 | 2.0 | 716 | 9 | AU133639 |
| c | 125 | 2.0 | 716 | 9 | AU133639 |
| c | 126 | 2.0 | 716 | 9 | AU133639 |
| c | 127 | 2.0 | 716 | 9 | AU133639 |
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http://www.tigr.org/tldb/humgen/bac_end_search/bac_end_search.html.

Seq primer: M13-21

Class: BAC ends.

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Db 139 AATACAGTCACTGACTCCACTTC 161

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DEFINITION AGENCOURT.6439488 NIH_MCC_71 Homo sapiens cDNA clone IMAGE:5520605
5', mRNA sequence.

ACCESSION BM803905

VERSION BM803905.1 GI:19120728

KEYWORDS EST.

SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

Plate: LLM12184 row: o column: 06

High quality sequence stop: 453.

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DEFINITION CM3-GN0313-050101-593-e06 GN0313 Homo sapiens cDNA, mRNA sequence.
ACCESSION BI050480
VERSION BI050480.1 GI:14458010
KEYWORDS EST.
SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE

AUTHORS 1 (bases 1 to 285)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Kagal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.

TITLE

Shotgun sequencing of the human transcriptome with ORF expressed

JOURNAL

sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE

20202663

COMMENT

Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=CM3&t2=CM3-GN0313-
050101-593-e06&t3=2001-01-05&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 8

High quality sequence stop: 285.

FEATURES

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application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the puc 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."

BASE COUNT 73 a 70 c 53 g 89 t

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Db 173 GACAAAGTCTGTCTGGGAC 154

RESULT 4

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DEFINITION RPC111-34118-TK RPC1-11 Homo sapiens genomic clone RPCI-11-34118,
DNA sequence.

ACCESSION

AQ046343

VERSION

AQ046343.1 GI:3315270

KEYWORDS

GSS.

SOURCE

human.

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 12, 2002, 05:32:20 ; Search time 79 Seconds

(without alignments)
7488.348 Million cell updates/sec

Title: US-09-771-045A-35

Perfect score: 1929

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Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

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; Patent No. 6211434
; GENERAL INFORMATION:
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
; FILE REFERENCE: 1134
; CURRENT APPLICATION NUMBER: US/09/352,159A
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: 60/092,936
; EARLIER FILING DATE: 1998-07-25
; EARLIER APPLICATION NUMBER: 60/135,391
; EARLIER FILING DATE: 1999-05-21
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Db 1381 CCTCTTCCCGCCGAGAGCAAGCATTTGGCGGAAAAATCTATCTCGGCTACTATACCAAG 1440
QY 1441 ATAGTCTTCGTATGGGACAAACCGTGGTGGCGGAAACAGGCTTCTCGGCGCTCTCCAA 1500
Db 1441 ATAGTCTTCGTATGGGACAAACCGTGGTGGCGGAAACAGGCTTCTCGGCGCTCTCCAA 1500
QY 1501 TCGAGCTGTGACCCCACTCTCATTTGCCAGAGATACCAAGCATCGAAGTCGATCGCAATGG 1560
Db 1501 TCGAGCTGTGACCCCACTCTCATTTGCCAGAGATACCAAGCATCGAAGTCGATCGCAATGG 1560
QY 1561 TCCATTACCTGTTTCATGGTTCGAGAGCCCGGAGGAAAGTGGTCCCAACAGTCCAAAGCAG 1620
Db 1561 TCCATTACCTGTTTCATGGTTCGAGAGCCCGGAGGAAAGTGGTCCCAACAGTCCAAAGCAG 1620
QY 1621 GTACGACAAAGTCTGTCTGGGACCAACTCCGCGAGCCCTACGAGAACGCGGGGCCCAA 1680
Db 1621 GTACGACAAAGTCTGTCTGGGACCAACTCCGCGAGCCCTACGAGAACGCGGGGCCCAA 1680
QY 1681 GTCCAGAGCCCGGCAACGCTCTCGAAATCGAGTGTGCGAAGCAGCAGTATTTCCAAAGGA 1740
Db 1681 GTCCAGAGCCCGGCAACGCTCTCGAAATCGAGTGTGCGAAGCAGCAGTATTTCCAAAGGA 1740
QY 1741 GCTCCGAGCGGCTCTATGGCTGAACGATCTCATCACACTGGGTTTCGCGCTCAAGACG 1800
Db 1741 GCTCCGAGCGGCTCTATGGCTGAACGATCTCATCACACTGGGTTTCGCGCTCAAGACG 1800
QY 1801 CCGTTCAAGTGTGTTTCATTTGTTGAAACGAGACGCTTTTACGTTTGGAAAGGTTATG 1860
Db 1801 CCGTTCAAGTGTGTTTCATTTCTGTTGAAACGAGACGCTTTTACGTTTGGAAAGGTTATG 1860
QY 1861 GAAGGGCCATACGATCGGTTCAACGAGTGTGCTGCAAGAGTTGTGCGTAGCCTGGTGCCA 1920
Db 1861 GAAGGGCCATACGATCGGTTCAACGAGTGTGCTGCAAGAGTTGTGCGTAGCCTGGTGCCA 1920
QY 1921 GCAGCATAG 1929
Db 1921 GCAGCATAG 1929
RESULT 2
US-09-352-159-37
; Sequence 37, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
; APPLICANT: Duivick, Jonathan P.
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; FILE REFERENCE: 1134
; CURRENT APPLICATION NUMBER: US/09/352.159A
; EARLIER FILING DATE: 1999-07-12
; EARLIER FILING DATE: 1998-07-25
; EARLIER FILING DATE: 1998-07-25
; EARLIER FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 37
; LENGTH: 1929
; TYPE: DNA
; ORGANISM: Exophiala spinifera
; FEATURE:
; NAME/KEY: intron
; LOCATION: (739)...(811)
; NAME/KEY: intron
; LOCATION: (1134)...(1186)
US-09-352-159-37

| | | | | | | | | | |
|---|-----|--|------|--|--|--|--|--|--|
| Query Match | | | | | | | | | |
| Best Local Similarity 94.7%; Score 1827; DB 4; Length 1929; | | | | | | | | | |
| Matches 1927; Conservative 0; Mismatches 2; Indels 0; Gaps 0; | | | | | | | | | |
| QY | 1 | ATGGCAGCTTGACCCAGCTACATCAATCCCCCAACAGTCGCGCTCCCCAGAGGGTATTCC | 60 | | | | | | |
| DB | 1 | ATGGCAGCTTGACCCAGCTACATCAATCCCCCAACAGTCGCGCTCCCCAGAGGGTATTCC | 60 | | | | | | |
| QY | 61 | CACATCGGGTAGGCGCCAAACGAGGATGTGACAAATGAGTGGACAGATTGGACAA | 120 | | | | | | |
| DB | 61 | CACATCGGGTAGGCGCCAAACGAGGATGTGACAAATGAGTGGACAGATTGGACAA | 120 | | | | | | |
| QY | 121 | GACGCTTTGGGCGTGACAGACCCAGCTTACGAGAAACAGGTTGCCAAAGCATTTGCCCAAT | 180 | | | | | | |
| DB | 121 | GACGCTTTGGGCGTGACAGACCCAGCTTACGAGAAACAGGTTGCCAAAGCATTTGCCCAAT | 180 | | | | | | |
| QY | 181 | CTGGCAGCTTGCTTGTGCTGAGTGGAGCCTTCAACAGAGCTCACCAAGCTCAATTAC | 240 | | | | | | |
| DB | 181 | CTGGCAGCTTGCTTGTGCTGAGTGGAGCCTTCAACAGAGCTCACCAAGCTCAATTAC | 240 | | | | | | |
| QY | 241 | TACATCGTGCAGCTAGCGCCCGGAGCAAACTCACCGCAATTTGGAGATGGCTGAAGTCTACC | 300 | | | | | | |
| DB | 241 | TACATCGTGCAGCTAGCGCCCGGAGCAAACTCACCGCAATTTGGAGATGGCTGAAGTCTACC | 300 | | | | | | |
| QY | 301 | TTTGCCCTTGACAGGCTCCCTCTTGCACGCTGTGCCAGTACCGGCTTGGCTTACCT | 360 | | | | | | |
| DB | 301 | TTTGCCCTTGACAGGCTCCCTCTTGCACGCTGTGCCAGTACCGGCTTGGCTTACCT | 360 | | | | | | |
| QY | 361 | GAATACCTTTGAGTTGATGCCAGCGGCTGTGCCAGACACTCAACCCAGACAAAC | 420 | | | | | | |
| DB | 361 | GAATACCTTTGAGTTGATGCCAGCGGCTGTGCCAGACACTCAACCCAGACAAAC | 420 | | | | | | |
| QY | 421 | GTTCGGAGCTGTAGTGTGGGCGCTGGCTTGTAGCGGTTTGGAGCGGACGCAAGATC | 480 | | | | | | |
| DB | 421 | GTTCGGAGCTGTAGTGTGGGCGCTGGCTTGTAGCGGTTTGGAGCGGACGCAAGATC | 480 | | | | | | |
| QY | 481 | CAGGCGCGGCTGTCTCTGCTGCTCTTGTAGGCGGATGGATCGTGTAGGGGAAAGACT | 540 | | | | | | |
| DB | 481 | CAGGCGCGGCTGTCTCTGCTGCTCTTGTAGGCGGATGGATCGTGTAGGGGAAAGACT | 540 | | | | | | |
| QY | 541 | CTGAGGTACATCGGTCGCGGAGGAGGACTATCAACAGACTTCGCGGCTGCGTGGATC | 600 | | | | | | |
| DB | 541 | CTGAGGTACATCGGTCGCGGAGGAGGACTATCAACAGACTTCGCGGCTGCGTGGATC | 600 | | | | | | |
| QY | 601 | AATGACAGCAACAAAGCGAAGTATCCAGATTGTTGAAAGATTTCATTTGGAGGGCGAG | 660 | | | | | | |
| DB | 601 | AATGACAGCAACAAAGCGAAGTATCCAGATTGTTGAAAGATTTCATTTGGAGGGCGAG | 660 | | | | | | |
| QY | 661 | CTCCAGAGGACGACCGGAAATTCATTCATCAAGCACAGAGCGGTACAAACACTACAGCT | 720 | | | | | | |
| DB | 661 | CTCCAGAGGACGACCGGAAATTCATTCATCAAGCACAGAGCGGTACAAACACTACAGCT | 720 | | | | | | |
| QY | 721 | CCTTATGCTGACTCCCGGTAGACACATCCCACTTTGTGATGAGACCTCTGTGAGTGT | 780 | | | | | | |
| DB | 721 | CCTTATGCTGACTCCCGGTAGACACATCCCACTTTGTGATGAGACCTCTGTGAGTGT | 780 | | | | | | |
| QY | 781 | AGAATACAGTCACTGACTCCACTTCGCTCCAGCTGAGCGAGGAGTTGCAAGTGCACTTGC | 840 | | | | | | |
| DB | 781 | AGAATACAGTCACTGACTCCACTTCGCTCCAGCTGAGCGAGGAGTTGCAAGTGCACTTGC | 840 | | | | | | |
| QY | 841 | GGAATCTCTCCCGTATGGTCTGATCGAAGAGTATAGCCTTTGAAGACCCCAAGGC | 900 | | | | | | |
| DB | 841 | GGAATCTCTCCCGTATGGTCTGATCGAAGAGTATAGCCTTTGAAGACCCCAAGGC | 900 | | | | | | |
| QY | 901 | GAGCCTCAGGCGAGCGGCTCGACATGTGAGCTTCGCGCACTACTGTGAGAAGGACCT | 960 | | | | | | |
| DB | 901 | GAGCCTCAGGCGAGCGGCTCGACATGTGAGCTTCGCGCACTACTGTGAGAAGGACCT | 960 | | | | | | |
| QY | 961 | AAACTTGCTGCTGTCTCAGCGTGGCAAAACAGATCAACGCGCTCTGCTCGGTTGGA | 1020 | | | | | | |
| DB | 961 | AAACTTGCTGCTGTCTCAGCGTGGCAAAACAGATCAACGCGCTCTGCTCGGTTGGA | 1020 | | | | | | |

| | | | | | | | | | |
|----|------|--|------|--|--|--|--|--|--|
| QY | 1021 | AGCCACGAGATCAGCATGCTTTTTCTCACGACTACATCAAGAGTGCACCGGTCTCAG | 1080 | | | | | | |
| DB | 1021 | AGCCACGAGATCAGCATGCTTTTTCTCACGACTACATCAAGAGTGCACCGGTCTCAG | 1080 | | | | | | |
| QY | 1081 | TAATATTGCTCGACAGAAAGACGGCGGAGTATATCGGATGCAAAACAGGTGCGTG | 1140 | | | | | | |
| DB | 1081 | TAATATTGCTCGGCAAGAAAGACGGCGGAGTATATCGGATGCAAAACAGGTGCGTG | 1140 | | | | | | |
| QY | 1141 | CGGTGCTCTCAGGTAGGGACTCGTTTCTTAGTGTCATTCCAGGTATGCAGTCAATT | 1200 | | | | | | |
| DB | 1141 | CGGTGCTCTCAGGTAGGGACTCGTTTCTTAGTGTCATTCCAGGTATGCAGTCAATT | 1200 | | | | | | |
| QY | 1201 | TGCCATGCCATGTCAAAGAACTTGTTCAGGCTCAGTCACCTCAACACCCCGTCGCT | 1260 | | | | | | |
| DB | 1201 | TGCCATGCCATGTCAAAGAACTTGTTCAGGCTCAGTCACCTCAACACCCCGTCGCT | 1260 | | | | | | |
| QY | 1261 | GGAATGAGCAGTCGGGCTCCGCTGTATAGTACGATCGGCTCGGGCGCGGTTCGGA | 1320 | | | | | | |
| DB | 1261 | GGAATGAGCAGTCGGGCTCCGCTGTATAGTACGATCGGCTCGGGCGCGGTTCGGA | 1320 | | | | | | |
| QY | 1321 | AGCAAAAAGTGTGTTCGTTACCGACAACATTTGTATCCCACTTGACATTTTCAACA | 1380 | | | | | | |
| DB | 1321 | AGCAAAAAGTGTGTTCGTTACCGACAACATTTGTATCCCACTTGACATTTTCAACA | 1380 | | | | | | |
| QY | 1381 | CCTCTTCCCGCGAGAAAGCAATTTGGCGGAAAAATCTATCTCGGCTACTATAGCAAG | 1440 | | | | | | |
| DB | 1381 | CCTCTTCCCGCGAGAAAGCAATTTGGCGGAAAAATCTATCTCGGCTACTATAGCAAG | 1440 | | | | | | |
| QY | 1441 | ATAGTCTTGTATGGGCAACCCGTTGGTGGCGGCAAGAGCTTCTCGGGCTCTCCAA | 1500 | | | | | | |
| DB | 1441 | ATAGTCTTGTATGGGCAACCCGTTGGTGGCGGCAAGAGCTTCTCGGGCTCTCCAA | 1500 | | | | | | |
| QY | 1501 | TCGAGCTGTACCCCACTCTCATTTGCCAGAGATACCAGCATCGAAGTCGATCGCAATGG | 1560 | | | | | | |
| DB | 1501 | TCGAGCTGTACCCCACTCTCATTTGCCAGAGATACCAGCATCGAAGTCGATCGCAATGG | 1560 | | | | | | |
| QY | 1561 | TCCATTACCTGTTTCATGTCGGAGACCCGGAGTGGTCCCAACAGTCCCAAGCAG | 1620 | | | | | | |
| DB | 1561 | TCCATTACCTGTTTCATGTCGGAGACCCGGAGTGGTCCCAACAGTCCCAAGCAG | 1620 | | | | | | |
| QY | 1621 | GTACGACAAAAGTCTGTCTGGGACCAACTCCGGCGAGCTTACGAGAACGCCGGGCCAA | 1680 | | | | | | |
| DB | 1621 | GTACGACAAAAGTCTGTCTGGGACCAACTCCGGCGAGCTTACGAGAACGCCGGGCCAA | 1680 | | | | | | |
| QY | 1681 | GTCCAGAGCGCGCAACAGTCTCGAAATCGAGTGTGCGAAGCAGCAGTATTTCCAAGGA | 1740 | | | | | | |
| DB | 1681 | GTCCAGAGCGCGCAACAGTCTCGAAATCGAGTGTGCGAAGCAGCAGTATTTCCAAGGA | 1740 | | | | | | |
| QY | 1741 | GCTCCGAGCGCGCTCTATGGGCTGAACGATCTCATCAGCTGGGTTTCGGCGCTCAGAAGC | 1800 | | | | | | |
| DB | 1741 | GCTCCGAGCGCGCTCTATGGGCTGAACGATCTCATCAGCTGGGTTTCGGCGCTCAGAAGC | 1800 | | | | | | |
| QY | 1801 | CCGTTCAAGTGTGTTTCATTTGGAACGAGACGCTTTTAGTTTGGAAAGGTATATG | 1860 | | | | | | |
| DB | 1801 | CCGTTCAAGTGTGTTTCATTTGGAACGAGACGCTTTTAGTTTGGAAAGGTATATG | 1860 | | | | | | |
| QY | 1861 | GAAAGGCGCATACGATCGGCTCAACGAGGTGCTCGAAGTTCGTGCTAGCCTGGTGCCA | 1920 | | | | | | |
| DB | 1861 | GAAAGGCGCATACGATCGGCTCAACGAGGTGCTCGAAGTTCGTGCTAGCCTGGTGCCA | 1920 | | | | | | |
| QY | 1921 | GCAGCATAG 1929 | | | | | | | |
| DB | 1921 | GCAGCATAG 1929 | | | | | | | |

RESULT 3
US-09-352-159-5
; Sequence 5, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
; APPLICANT: Duwick, Jonathan P.
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.


```
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; FILE REFERENCE: 1134
; CURRENT APPLICATION NUMBER: US/09/352,159A
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: 60/092,936
; EARLIER FILING DATE: 1998-07-25
; EARLIER APPLICATION NUMBER: 60/135,391
; EARLIER FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 1389
; TYPE: DNA
; ORGANISM: Exophiala spinifera
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1386)
US-09-352-159-5

Query Match
Best Local Similarity 16.8%; Score 324; DB 4; Length 1389;
Matches 374; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1555 CAATGGTCCATTACCTGTTTCATGTCGGAGACCGCGGACGGAAGTGTCTCCCAACAGTCC 1614
Db 1015 CAATGGTCCATTACCTGTTTCATGTCGGAGACCGCGGACGGAAGTGTCTCCCAACAGTCC 1074

QY 1615 AAGCAGGTACGACAAAAGTCTGTCTGGGACCAACTCCGCGCAGCCTACGAGAACGCCGGG 1674
Db 1675 AAGCAGGTACGACAAAAGTCTGTCTGGGACCAACTCCGCGCAGCCTACGAGAACGCCGGG 1134

QY 1675 GCCCAAGTCCCGAGCGCGCCACGTCGCTGAAATCGAGTGTGCGAAGCAGTATTTC 1734
Db 1135 GCCCAAGTCCCGAGCGCGCCACGTCGCTGAAATCGAGTGTGCGAAGCAGTATTTC 1194

QY 1735 CAAGAGTCCGAGCGCCCTCTATGGGTCGAAATCGAGTGTGCGAAGTGTGCGGCGCTC 1794
Db 1195 CAAGAGTCCGAGCGCCCTCTATGGGTCGAAATCGAGTGTGCGAAGTGTGCGGCGCTC 1254

QY 1795 AGAACCCGCTCAAGTGTCTTCAATTCGTTGGAACGAGACGCTTTAGTTTGGAAAGG 1854
Db 1255 AGAACCCGCTCAAGTGTCTTCAATTCGTTGGAACGAGACGCTTTAGTTTGGAAAGG 1314

QY 1855 TATATGGAAGGGCCATACGATCGGTCAACGAGTGTCTGCAAGTGTGTGCTAGCCTG 1914
Db 1315 TATATGGAAGGGCCATACGATCGGTCAACGAGTGTCTGCAAGTGTGTGCTAGCCTG 1374

QY 1915 GTGCCAGCAGCATAG 1929
Db 1375 GTGCCAGCAGCATAG 1389

RESULT 4
US-09-352-168-5
; Sequence 5, Application US/09352168A
; Patent No. 6211435
; GENERAL INFORMATION:
; APPLICANT: Crusta, Oswald R.
; APPLICANT: Duveck, Jonathan P.
; APPLICANT: Folkerts, Otto
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; FILE REFERENCE: 0875
; CURRENT APPLICATION NUMBER: US/09/352,168A
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: 60/092,936
; EARLIER FILING DATE: 1998-07-25
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
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; LENGTH: 1389
; TYPE: DNA
; ORGANISM: Exophiala spinifera
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1386)
US-09-352-168-5

Query Match
Best Local Similarity 16.8%; Score 324; DB 4; Length 1389;
Matches 374; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1555 CAATGGTCCATTACCTGTTTCATGTCGGAGACCGCGGACGGAAGTGTCTCCCAACAGTCC 1614
Db 1015 CAATGGTCCATTACCTGTTTCATGTCGGAGACCGCGGACGGAAGTGTCTCCCAACAGTCC 1074

QY 1615 AAGCAGGTACGACAAAAGTCTGTCTGGGACCAACTCCGCGCAGCCTACGAGAACGCCGGG 1674
Db 1075 AAGCAGGTACGACAAAAGTCTGTCTGGGACCAACTCCGCGCAGCCTACGAGAACGCCGGG 1134

QY 1675 GCCCAAGTCCCGAGCGCGCCACGTCGCTGAAATCGAGTGTGCGAAGCAGTATTTC 1734
Db 1135 GCCCAAGTCCCGAGCGCGCCACGTCGCTGAAATCGAGTGTGCGAAGCAGTATTTC 1194

QY 1735 CAAGAGTCCGAGCGCCCTCTATGGGTCGAAATCGAGTGTGCGAAGTGTGCGGCGCTC 1794
Db 1195 CAAGAGTCCGAGCGCCCTCTATGGGTCGAAATCGAGTGTGCGAAGTGTGCGGCGCTC 1254

QY 1795 AGAACCCGCTCAAGTGTCTTCAATTCGTTGGAACGAGACGCTTTAGTTTGGAAAGG 1854
Db 1255 AGAACCCGCTCAAGTGTCTTCAATTCGTTGGAACGAGACGCTTTAGTTTGGAAAGG 1314

QY 1855 TATATGGAAGGGCCATACGATCGGTCAACGAGTGTCTGCAAGTGTGTGCTAGCCTG 1914
Db 1315 TATATGGAAGGGCCATACGATCGGTCAACGAGTGTCTGCAAGTGTGTGCTAGCCTG 1374

QY 1915 GTGCCAGCAGCATAG 1929
Db 1375 GTGCCAGCAGCATAG 1389

RESULT 5
US-09-352-159-10
; Sequence 10, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
; APPLICANT: Duveck, Jonathan P.
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; FILE REFERENCE: 1134
; CURRENT APPLICATION NUMBER: US/09/352,159A
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: 60/092,936
; EARLIER FILING DATE: 1998-07-25
; EARLIER APPLICATION NUMBER: 60/135,391
; EARLIER FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 1392
; TYPE: DNA
; ORGANISM: Exophiala spinifera
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1389)
; NAME/KEY: misc_feature
; LOCATION: (1)...(3)
; OTHER INFORMATION: Extra lysine in K:trAPAQ
US-09-352-159-10

Query Match
Best Local Similarity 16.8%; Score 324; DB 4; Length 1392;
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Db 1248 CAAGGAGTCCGAGCGCGTCTATGGCTGAACGATCTCATCACACTGGTTTCGGCGCTC 1307
QY 1795 AGAAGCGGTTCAAGTGTGTTCAATTCGTTGGAACGAGACGCTCTTTAGTTGGAAAGG 1854
Db 1308 AGAAGCGGTTCAAGAGTGTGTTCAATTCGTTGGAACGAGACGCTCTTTAGTTGGAAAGG 1367
QY 1855 TATATGGAAGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAAGTTGTGGCTAGCCTG 1914
Db 1368 TATATGGAAGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAAGTTGTGGCTAGCCTG 1427
QY 1915 GTGCCAGCAGCATAG 1929
Db 1428 GTGCCAGCAGCATAG 1442

RESULT 8
US-09-352-168-7
; Sequence 7, Application US/09352168A
; Patent No. 6211435
; GENERAL INFORMATION:
; APPLICANT: Crasta, Oswald R.
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: Folkerts, Otto
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; FILE REFERENCE: 0875
; CURRENT APPLICATION NUMBER: US/09/352,168A
; EARLIER FILING DATE: 1999-07-12
; EARLIER FILING DATE: 1998-07-25
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 1442
; TYPE: DNA
; ORGANISM: Exophiala spinifera
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(646)
; NAME/KEY: intron
; LOCATION: (647)...(699)
; NAME/KEY: CDS
; LOCATION: (700)...(1439)
US-09-352-168-7

Query Match 16.8%; Score 324; DB 4; Length 1442;
Best Local Similarity 99.7%; Pred. No. 3.3e-159;
Matches 374; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1555 CAATGGTCCATTACCTGTTTCATGGTCCGAGACCCGGGACGGAAGTGTCCCAACAGTCC 1614
Db 1068 CAATGGTCCATTACCTGTTTCATGGTCCGAGACCCGGGACGGAAGTGTCCCAACAGTCC 1127
QY 1615 AAGCAGGTACGACAAAAGTCTGTCTGGAGCACTCCGCGACGCTACGAGAACGCCGG 1674
Db 1128 AAGCAGGTACGACAAAAGTCTGTCTGGAGCACTCCGCGACGCTACGAGAACGCCGG 1187
QY 1675 GCCCAAGTCCAGAGCCGGGCAACGTCGCTCGAAATCGAGTGTGCGAAGCAGCATTTTC 1734
Db 1188 GCCCAAGTCCAGAGCCGGGCAACGTCGCTCGAAATCGAGTGTGCGAAGCAGCATTTTC 1247
QY 1735 CAAGGAGCTCCGAGCGCGTCTATGGCTGAACGATCTCATCACACTGGTTTCGGCGCTC 1794
Db 1248 CAAGGAGCTCCGAGCGCGTCTATGGCTGAACGATCTCATCACACTGGTTTCGGCGCTC 1307
QY 1795 AGAAGCGGTTCAAGTGTGTTCAATTCGTTGGAACGAGACGCTCTTTAGTTGGAAAGG 1854
Db 1308 AGAAGCGGTTCAAGAGTGTGTTCAATTCGTTGGAACGAGACGCTCTTTAGTTGGAAAGG 1367
QY 1855 TATATGGAAGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAAGTTGTGGCTAGCCTG 1914
Db 1368 TATATGGAAGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAAGTTGTGGCTAGCCTG 1427
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Db 1368 TATATGGAAGGGCCATACGATCGGGTCAACGAGGTGCTGCAGAAAGTTGTGGCTAGCCTG 1427
QY 1915 GTGCCAGCAGCATAG 1929
Db 1428 GTGCCAGCAGCATAG 1442

RESULT 9
US-09-352-159-20
; Sequence 20, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; FILE REFERENCE: 1134
; CURRENT APPLICATION NUMBER: US/09/352,159A
; EARLIER FILING DATE: 1999-07-12
; EARLIER FILING DATE: 1998-07-25
; EARLIER FILING DATE: 1998-07-25
; EARLIER FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 1464
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Nucleotide sequence of K:trPAO translational
; OTHER INFORMATION: fusion with barley alpha amylase signal sequence.
; OTHER INFORMATION: for expression and secretion of the mature trPAO
; OTHER INFORMATION: in maize. Nucleotides 1-72, Barley alpha amylase
; OTHER INFORMATION: signal sequence, nucleotides 73-75, added lysine
; OTHER INFORMATION: residue; nucleotides 76 -1464 , trPAO cDNA.
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (1)...(72)
; OTHER INFORMATION: Barley alpha amylase signal sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (73)...(1464)
; OTHER INFORMATION: K:trPAOcDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1461)
; NAME/KEY: misc_feature
; LOCATION: (73)...(75)
; OTHER INFORMATION: Added lysine residue
US-09-352-159-20

Query Match 16.8%; Score 324; DB 4; Length 1464;
Best Local Similarity 99.7%; Pred. No. 3.3e-159;
Matches 374; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1555 CAATGGTCCATTACCTGTTTCATGGTCCGAGACCCGGGACGGAAGTGTCCCAACAGTCC 1614
Db 1090 CAATGGTCCATTACCTGTTTCATGGTCCGAGACCCGGGACGGAAGTGTCCCAACAGTCC 1149
QY 1615 AAGCAGGTACGACAAAAGTCTGTCTGGAGCACTCCGCGACGCTACGAGAACGCCGG 1674
Db 1150 AAGCAGGTACGACAAAAGTCTGTCTGGAGCACTCCGCGACGCTACGAGAACGCCGG 1209
QY 1675 GCCCAAGTCCAGAGCCGGGCAACGTCGCTCGAAATCGAGTGTGCGAAGCAGCATTTTC 1734
Db 1210 GCCCAAGTCCAGAGCCGGGCAACGTCGCTCGAAATCGAGTGTGCGAAGCAGCATTTTC 1269
QY 1735 CAAGGAGCTCCGAGCGCGTCTATGGCTGAACGATCTCATCACACTGGTTTCGGCGCTC 1794
Db 1270 CAAGGAGCTCCGAGCGCGTCTATGGCTGAACGATCTCATCACACTGGTTTCGGCGCTC 1329
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QY 1795 AGAACCCGCTTCAAGTGTTCATTTCTGTTGGAACGGAGACGCTCTTATAGTTTGGAAAGGG 1854
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Db 1330 AGAACCCGCTTCAAGAGTCTTCAATTTCTGTTGGAACGGAGACGCTCTTATAGTTTGGAAAGGG 1389
|||||
QY 1855 TATATGGAAGGGCCATACGATCGGGTCAACGAGTGTCTGAGAAGTTGTGGCTAGCCCTG 1914
|||||
Db 1390 TATATGGAAGGGCCATACGATCGGGTCAACGAGTGTCTGAGAAGTTGTGGCTAGCCCTG 1449
|||||
QY 1915 GTGCCAGCAGCATAG 1929
|||||
Db 1450 GTGCCAGCAGCATAG 1464
|||||
RESULT 10
US-09-352-168-20
; Sequence 20, Application US/09352168A
; Patent No. 6211435
; GENERAL INFORMATION:
; APPLICANT: Crasta, Oswald R.
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: Folkerts, Otto
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
; FILE REFERENCE: 0875
; CURRENT APPLICATION NUMBER: US/09/352.168A
; EARLIER FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: 60/092,936
; EARLIER FILING DATE: 1998-07-25
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 1464
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (1)...(72)
; OTHER INFORMATION: Barley Alpha Amylase signal sequence.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (73)...(1464)
; OTHER INFORMATION: K:trAPOcDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1461)
; OTHER INFORMATION: Nucleotide sequence of K:trAPO translational
; OTHER INFORMATION: fusion with barley alpha amylase signal sequence,
; OTHER INFORMATION: for expression and secretion of the mature trAPO
; OTHER INFORMATION: in maize. Nucleotides 1-72, barley alpha amylase
; OTHER INFORMATION: signal sequence, nucleotides 73-75, added lysine
; OTHER INFORMATION: residue; nucleotides 76-1464, trAPO cDNA.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (73)...(75)
; OTHER INFORMATION: Added lysine residue
US-09-352-168-20
Query Match 16.8%; Score 324; DB 4; Length 1464;
Best Local Similarity 99.7%; Pred. No. 3.3e-159;
Matches 374; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 1090 CAATGGTCCATTACCTGTTTCATGTCGGAGACCCGGAGCGGAAGTGGTCCCAACAGTCC 1149
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QY 1615 AAGCAGGTACGACAAAAGTCTGTCTGGGACCAACTCCGCGCAGCCTACGAGAACGCCGG 1674
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Db 1150 AAGCAGGTACGACAAAAGTCTGTCTGGGACCAACTCCGCGCAGCCTACGAGAACGCCGG 1209
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QY 1675 GCCCAAGTCCAGAGCCGCCAACGTCGTAATCGAGTGGTCTGGAAGGAGCAGTATTTTC 1734
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Db 1210 GCCCAAGTCCAGAGCCGCCAACGTCGTAATCGAGTGGTCTGGAAGCAGCAGTATTTTC 1269
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QY 1735 CAAGGAGCTCGGAGCCGCCCTGCTATGGGCTGAACGATCTCATCACACTGGGTTCCGGCGCTC 1794
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Db 1270 CAAGGAGCTCGGAGCCGCCCTGCTATGGGCTGAACGATCTCATCACACTGGGTTCCGGCGCTC 1329
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QY 1795 AGAACCCGCTTCAAGTGTTCATTTCTGTTGGAACGGAGACGCTCTTATAGTTTGGAAAGGG 1854
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Db 1330 AGAACCCGCTTCAAGAGTGTTCATTTCTGTTGGAACGGAGACGCTCTTATAGTTTGGAAAGGG 1389
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QY 1855 TATATGGAAGGGCCATACGATCGGGTCAACGAGTGTCTGAGAAGTTGTGGCTAGCCCTG 1914
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QY 1915 GTGCCAGCAGCATAG 1929
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Db 1450 GTGCCAGCAGCATAG 1464
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RESULT 11
US-09-352-159-16
; Sequence 16, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
; FILE REFERENCE: 1134
; CURRENT APPLICATION NUMBER: US/09/352.159A
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: 60/092,936
; EARLIER FILING DATE: 1998-07-25
; EARLIER APPLICATION NUMBER: 60/135,391
; EARLIER FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 1673
; TYPE: DNA
; ORGANISM: Exophiala spinifera
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (1)...(267)
; OTHER INFORMATION: Yeast alpha mating factor secretion signal.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1662)
US-09-352-159-16
Query Match 16.8%; Score 324; DB 4; Length 1673;
Best Local Similarity 99.7%; Pred. No. 3.3e-159;
Matches 374; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 1291 CAATGGTCCATTACCTGTTTCATGTCGGAGACCCGGAGCGGAAGTGGTCCCAACAGTCC 1350
|||||
QY 1615 AAGCAGGTACGACAAAAGTCTGTCTGGGACCAACTCCGCGCAGCCTACGAGAACGCCGG 1674
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Db 1351 AAGCAGGTACGACAAAAGTCTGTCTGGGACCAACTCCGCGCAGCCTACGAGAACGCCGG 1410
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QY 1675 GCCCAAGTCCAGAGCCGCCAACGTCGTAATCGAGTGGTCTGGAAGGAGCAGTATTTTC 1734
|||||
Db 1411 GCCCAAGTCCAGAGCCGCCAACGTCGTAATCGAGTGGTCTGGAAGGAGCAGTATTTTC 1470
|||||
QY 1735 CAAGGAGCTCCGAGCCGCCCTGCTATGGGCTGAACGATCTCATCACACTGGGTTCCGGCGCTC 1794
|||||
Db 1471 CAAGGAGCTCCGAGCCGCCCTGCTATGGGCTGAACGATCTCATCACACTGGGTTCCGGCGCTC 1530
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QY 1795 AGAACCCGCTTCAAGTGTTCATTTCTGTTGGAAGGAGCAGCCTCTTATAGTTTGGAAAGGG 1854
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Db 1531 AGAACCCGTTCAAGAGTGTTCATTTGCTTGGACGGAGACGCTTTAGTTTGGAAAGG 1590
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Db 1591 TATATGGAAGGGCCATAGATCGGTCAACAGAGTGTGCAGAAAGTTGTGCTAGCCTG 1650
Qy 1915 GTGCCAGCAGCATAG 1929
Db 1651 GTGCCAGCAGCATAG 1665

RESULT 12
US-09-352-168-16
; Sequence 16, Application US/09352168A
; Patent No. 6211435
; GENERAL INFORMATION:
; APPLICANT: Crasta, Oswald R.
; APPLICANT: Duviok, Jonathan P.
; APPLICANT: Folkerts, Otto
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
; FILE REFERENCE: 0875
; CURRENT APPLICATION NUMBER: US/09/352,168A
; EARLIER FILING DATE: 1999-07-12
; EARLIER FILING DATE: 1998-07-25
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 1673
; TYPE: DNA
; ORGANISM: Exophiala spinifera
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (1)...(267)
; OTHER INFORMATION: yeast alpha mating factor secretion signal.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1662)
; US-09-352-168-16

Query Match 16.8%; Score 324; DB 4; Length 1673;
Best Local Similarity 99.7%; Pred. No. 3.3e-159;
Matches 374; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1555 CAATGTCATTACCTGTTTCATGTCGGAGACCCGGGACGGAAGTGTCCCAACAGTCC 1614
Db 1291 CAATGTCATTACCTGTTTCATGTCGGAGACCCGGGACGGAAGTGTCCCAACAGTCC 1350
Qy 1615 AAGCAGGTACGACAAAGTCTGTCGGACCAACTCCGCGACGCTACGAGAACGCCGGG 1674
Db 1351 AAGCAGGTACGACAAAGTCTGTCGGACCAACTCCGCGACGCTACGAGAACGCCGGG 1410
Qy 1675 GCCCAAGTCCAGAGCGGCGCAACGTGCTCGAAATCGAGTGTGCGAAGCAGAGTATTTTC 1734
Db 1411 GCCCAAGTCCAGAGCGGCGCAACGTGCTCGAAATCGAGTGTGCGAAGCAGAGTATTTTC 1470
Qy 1735 CAAGGAGTCCGAGCGCGCTCTATGGGTGAGCATCTCATCACACTGGGTTCGGCGCTC 1794
Db 1471 CAAGGAGTCCGAGCGCGCTCTATGGGTGAGCATCTCATCACACTGGGTTCGGCGCTC 1530
Qy 1795 AGAACCGGTTCAAGTGTGTTTCATTTGTTGGAACGGAGACGCTTTAGTTTGGAAAGG 1854
Db 1531 AGAACCGGTTCAAGTGTGTTTCATTTGTTGGAACGGAGACGCTTTAGTTTGGAAAGG 1590
Qy 1855 TATATGGAAGGGCCATAGATCGGTCAACAGAGTGTGCAGAAAGTTGTGCTAGCCTG 1914
Db 1591 TATATGGAAGGGCCATAGATCGGTCAACAGAGTGTGCAGAAAGTTGTGCTAGCCTG 1650
Qy 1915 GTGCCAGCAGCATAG 1929
Db 1651 GTGCCAGCAGCATAG 1665
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Db 1651 GTGCCAGCAGCATAG 1665

RESULT 13
US-09-352-159-22
; Sequence 22, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
; APPLICANT: Duviok, Jonathan P.
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polyol Amine Oxidase
; TITLE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
; FILE REFERENCE: 1134
; CURRENT APPLICATION NUMBER: US/09/352,159A
; CURRENT FILING DATE: 1999-07-12
; EARLIER FILING DATE: 1998-07-25
; EARLIER FILING DATE: 1998-07-25
; EARLIER FILING DATE: 1998-07-25
; EARLIER FILING DATE: 1998-07-25
; EARLIER FILING DATE: 1998-07-25
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 1803
; TYPE: DNA
; ORGANISM: Exophiala spinifera
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1800)
; US-09-352-159-22

Query Match 16.8%; Score 324; DB 4; Length 1803;
Best Local Similarity 99.7%; Pred. No. 3.3e-159;
Matches 374; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1795 AGAACCGGTTCAAGTGTGTTTCATTTGTTGGAACGGAGACGCTTTAGTTTGGAAAGG 1854
Db 1669 AGAACCGGTTCAAGTGTGTTTCATTTGTTGGAACGGAGACGCTTTAGTTTGGAAAGG 1728
Qy 1855 TATATGGAAGGGCCATAGATCGGTCAACAGAGTGTGCGAAGTGTGCGTAGCCTG 1914
Db 1729 TATATGGAAGGGCCATAGATCGGTCAACAGAGTGTGCGAAGTGTGCGTAGCCTG 1788
Qy 1915 GTGCCAGCAGCATAG 1929
Db 1789 GTGCCAGCAGCATAG 1803

RESULT 14
US-09-352-168-22
; Sequence 22, Application US/09352168A
; Patent No. 6211435
; GENERAL INFORMATION:
; APPLICANT: Crasta, Oswald R.
; APPLICANT: Duviok, Jonathan P.
; APPLICANT: Folkerts, Otto
; APPLICANT: Gilliam, Jacob T.
```

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; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polylol Amine Oxidase
; FILE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
; FILE REFERENCE: 0875
; CURRENT APPLICATION NUMBER: US/09/352,168A
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: 60/092,936
; EARLIER FILING DATE: 1998-07-25
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 1803
; TYPE: DNA
; ORGANISM: Exophiala spinifera
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)....(1800)
US-09-352-168-22

Query Match      16.8%; Score 324; DB 4; Length 1803;
Best Local Similarity 99.7%; Pred. No. 3.3e-159;
Matches 374; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 1429 CAATGTCATTACCTGTTTCATGTCGGAGACCCGGGACCGGAAGTGTGCCACACAGTCC 1488
QY 1615 AAGCAGGTACGACAAAGTCTCTCTGGACCAACTCCCGCGAGCCTACGAGAACGCCGGG 1674
Db 1489 AAGCAGGTACGACAAAGTCTCTCTGGACCAACTCCCGCGAGCCTACGAGAACGCCGGG 1548
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Db 1609 CAAGGAGCTCCGAGCGCCGCTCTATGGCTGAACGATCTCATCACACTCGGTTCCGGCGTC 1668
QY 1795 AGAACGCCGTTCAAGTGTGTTTCATTTCTGTTGGAACGGAGACGCTCTTTAGTTTGGAAAGG 1854
Db 1669 AGAACGCCGTTCAAGTGTGTTTCATTTCTGTTGGAACGGAGACGCTCTTTAGTTTGGAAAGG 1728
QY 1855 TATATGAAGGGGCCATACGATCGGTCACACGAGTGTGTCAGAGAAGTGTGCTAGCCTG 1914
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QY 1915 GTGCCAGCAGCATAG 1929
Db 1789 GTGCCAGCAGCATAG 1803

RESULT 15
US-09-352-159-39
; Sequence 39, Application US/09352159A
; Patent No. 6211434
; GENERAL INFORMATION:
; APPLICANT: Duvick, Jonathan P.
; APPLICANT: Gilliam, Jacob T.
; APPLICANT: Maddox, Joyce R.
; TITLE OF INVENTION: Amino Polylol Amine Oxidase
; FILE OF INVENTION: Polynucleotides and Related Polypeptides and Methods of Use
; FILE REFERENCE: 1134
; CURRENT APPLICATION NUMBER: US/09/352,159A
; CURRENT FILING DATE: 1999-07-12
; EARLIER APPLICATION NUMBER: 60/092,936
; EARLIER FILING DATE: 1998-07-25
; EARLIER APPLICATION NUMBER: 60/135,391
; EARLIER FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 39
; LENGTH: 1930
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; ORGANISM: Exophiala spinifera
; FEATURE:
; NAME/KEY: intron
; LOCATION: (739)....(811)
; NAME/KEY: intron
; LOCATION: (1134)....(1187)
; NAME/KEY: misc feature
; LOCATION: (648)....(648)
; OTHER INFORMATION: n = A,T,C or G
US-09-352-159-39

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Best Local Similarity 99.7%; Pred. No. 3.3e-159;
Matches 374; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1615 AAGCAGGTACGACAAAGTCTCTCTGGACCAACTCCCGCGAGCCTACGAGAACGCCGGG 1674
Db 1616 AAGCAGGTACGACAAAGTCTCTCTGGACCAACTCCCGCGAGCCTACGAGAACGCCGGG 1675
QY 1675 GCCAAGTCCGAGCGCGCCAACTGCTCGAATCGAGTGTGGAACGACGACGATATTC 1734
Db 1676 GCCAAGTCCGAGCGCGCCAACTGCTCGAATCGAGTGTGGAACGACGACGATATTC 1735
QY 1735 CAAGGAGCTCCGAGCGCCGCTCTATGGCTGAACGATCTCATCACACTCGGTTCCGGCGTC 1794
Db 1736 CAAGGAGCTCCGAGCGCCGCTCTATGGCTGAACGATCTCATCACACTCGGTTCCGGCGTC 1795
QY 1795 AGAACGCCGTTCAAGTGTGTTTCATTTCTGTTGGAACGGAGACGCTCTTTAGTTTGGAAAGG 1854
Db 1796 AGAACGCCGTTCAAGTGTGTTTCATTTCTGTTGGAACGGAGACGCTCTTTAGTTTGGAAAGG 1855
QY 1855 TATATGAAGGGGCCATACGATCGGTCACACGAGTGTGTCAGAGAAGTGTGCTAGCCTG 1914
Db 1856 TATATGAAGGGGCCATACGATCGGTCACACGAGTGTGTCAGAGAAGTGTGCTAGCCTG 1915
QY 1915 GTGCCAGCAGCATAG 1929
Db 1916 GTGCCAGCAGCATAG 1930

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Job time : 87 secs
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GenCore version 5.1.3
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Perfect score: 1929
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Gapop 60.0 , Gapext 60.0

Searched: 320260 seqs, 177392727 residues

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
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| 2 | 19 | 1.0 | 222 | 10 | US-09-833-263-887 |
| 3 | 19 | 1.0 | 228 | 10 | US-09-922-217-939 |
| 4 | 19 | 1.0 | 228 | 10 | US-09-833-263-939 |
| 5 | 17 | 0.9 | 239 | 10 | US-09-878-574-10314 |
| 6 | 17 | 0.9 | 261 | 10 | US-09-878-574-7447 |
| 7 | 17 | 0.9 | 264 | 10 | US-09-923-876-1462 |
| 8 | 17 | 0.9 | 433 | 10 | US-09-960-352-7464 |
| 9 | 17 | 0.9 | 443 | 10 | US-09-960-352-4610 |
| 10 | 17 | 0.9 | 476 | 10 | US-09-864-761-2462 |
| 11 | 17 | 0.9 | 597 | 10 | US-09-864-761-7247 |
| 12 | 17 | 0.9 | 610 | 10 | US-09-864-761-19193 |
| 13 | 17 | 0.9 | 826 | 10 | US-09-770-445-714 |
| 14 | 17 | 0.9 | 880 | 9 | US-09-938-842A-4623 |
| 15 | 17 | 0.9 | 1657 | 10 | US-09-925-301-134 |
| 16 | 17 | 0.9 | 1884 | 9 | US-09-938-842A-905 |
| 17 | 17 | 0.9 | 2247 | 10 | US-09-974-300-170 |
| 18 | 17 | 0.9 | 4719 | 9 | US-09-808-602-57 |
| 19 | 17 | 0.9 | 5502 | 9 | US-09-808-602-3 |

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|----|-----|-----|----|---------------------|-------------------|
| 16 | 0.8 | 77 | 10 | US-09-844-508-24 | Sequence 24, Appl |
| 16 | 0.8 | 83 | 9 | US-09-942-087A-26 | Sequence 26, Appl |
| 16 | 0.8 | 83 | 10 | US-09-779-233-14 | Sequence 14, Appl |
| 22 | 0.8 | 203 | 10 | US-09-960-352-12039 | Sequence 12039, A |
| 23 | 0.8 | 203 | 10 | US-09-923-876-3532 | Sequence 3532, Ap |
| 24 | 0.8 | 235 | 10 | US-09-960-352-12494 | Sequence 12494, A |
| 25 | 0.8 | 241 | 10 | US-09-960-352-12759 | Sequence 12759, A |
| 26 | 0.8 | 243 | 10 | US-09-923-876-3057 | Sequence 3057, Ap |
| 27 | 0.8 | 248 | 10 | US-09-960-352-5418 | Sequence 5418, Ap |
| 28 | 0.8 | 253 | 10 | US-09-923-876-1830 | Sequence 1830, Ap |
| 29 | 0.8 | 263 | 10 | US-09-923-876-515 | Sequence 515, App |
| 30 | 0.8 | 269 | 10 | US-09-923-876-515 | Sequence 2802, Ap |
| 31 | 0.8 | 331 | 10 | US-09-770-791-845 | Sequence 845, App |
| 32 | 0.8 | 340 | 10 | US-09-783-590-10561 | Sequence 10561, A |
| 33 | 0.8 | 348 | 10 | US-09-770-791-666 | Sequence 666, App |
| 34 | 0.8 | 353 | 10 | US-09-960-352-14899 | Sequence 14899, A |
| 35 | 0.8 | 380 | 10 | US-09-770-791-18 | Sequence 18, Appl |
| 36 | 0.8 | 390 | 10 | US-09-604-287A-227 | Sequence 227, App |
| 37 | 0.8 | 391 | 10 | US-09-339-338-227 | Sequence 227, App |
| 38 | 0.8 | 391 | 12 | US-10-007-805-227 | Sequence 227, App |
| 39 | 0.8 | 391 | 12 | US-09-864-761-23869 | Sequence 23869, A |
| 40 | 0.8 | 399 | 10 | US-09-960-352-1982 | Sequence 1982, Ap |
| 41 | 0.8 | 412 | 10 | US-09-960-352-9410 | Sequence 9410, Ap |
| 42 | 0.8 | 417 | 10 | US-09-783-590-2288 | Sequence 2288, Ap |
| 43 | 0.8 | 418 | 10 | US-09-960-352-9138 | Sequence 9138, Ap |
| 44 | 0.8 | 418 | 10 | US-09-867-701-5519 | Sequence 5519, Ap |
| 45 | 0.8 | 422 | 10 | | |

ALIGNMENTS

RESULT 1

US-09-922-217-887

; Sequence 887, Application US/09922217

; Patent No. US20020076414A1

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Lodes, Michael J.

; APPLICANT: Secrist, Heather

; APPLICANT: Benson, Darin R.

; APPLICANT: Meagher, Madeleine Joy

; APPLICANT: Stolk, John A.

; APPLICANT: Wang, Tongtong

; APPLICANT: Jiang, Yuqi

; APPLICANT: Smith, Carole Lynn

; APPLICANT: King, Gordon E.

; APPLICANT: Wang, Aijun

; APPLICANT: Clapper, Jonathan D.

; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS

; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE

; FILE REFERENCE: 210121.471C13

; CURRENT APPLICATION NUMBER: US/09/922,217

; CURRENT FILING DATE: 2001-08-03

; NUMBER OF SEQ ID NOS: 1124

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 887

; LENGTH: 222

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-922-217-887

Query Match 1.0%; Score 19; DB 10; Length 222;
Best Local Similarity 100.0%; Pred No. 1.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 170 CGCCGGGGCCCAAGTCCCA 188

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US-09-833-263-887

; Sequence 887, Application US/09833263


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; Patent No. US20020110547A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Stolk, John A.
; APPLICANT: Meagher, Madeleine J.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C12
; CURRENT APPLICATION NUMBER: US/09/833,263
; CURRENT FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 887
; LENGTH: 222
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-833-263-939

Query Match      1.0%; Score 19; DB 10; Length 222;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1668 CGCCGGGGCCCAAGTCCCA 1686
|||||
Db 170 CGCCGGGGCCCAAGTCCCA 188

RESULT 3
US-09-922-217-939
; Sequence 939, Application US/09922217
; Patent No. US20020076414A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Smith, Carole Lynn
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C13
; CURRENT APPLICATION NUMBER: US/09/922,217
; CURRENT FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 1124
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 939
; LENGTH: 228
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-922-217-939

Query Match      1.0%; Score 19; DB 10; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1668 CGCCGGGGCCCAAGTCCCA 1686
|||||
Db 170 CGCCGGGGCCCAAGTCCCA 188

RESULT 4
US-09-833-263-939
; Sequence 939, Application US/09833263
; Patent No. US20020110547A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Stolk, John A.
; APPLICANT: Meagher, Madeleine J.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C12
; CURRENT APPLICATION NUMBER: US/09/833,263
; CURRENT FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 887
; LENGTH: 222
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-833-263-939

Query Match      1.0%; Score 19; DB 10; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1668 CGCCGGGGCCCAAGTCCCA 1686
|||||
Db 170 CGCCGGGGCCCAAGTCCCA 188

RESULT 5
US-09-878-574-10314
; Sequence 10314, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 10314
; LENGTH: 239
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 701103537H1
; US-09-878-574-10314

Query Match      0.9%; Score 17; DB 10; Length 239;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 232 CTCAAATTACTACATCGT 248
|||||
Db 37 CTCAAATTACTACATCGT 53

RESULT 6
US-09-878-574-7447
; Sequence 7447, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
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; SEQ ID NO 7447
; LENGTH: 261
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 701099887H1
US-09-878-574-7447

Query Match          0.9%; Score 17; DB 10; Length 261;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 232 CTCGAATTACTACATCGT 248
      |||
Db 35 CTCGAATTACTACATCGT 51

RESULT 7
US-09-923-876-1462/c
; Sequence 1462, Application US/09923876
; Patent No. US20020013958A1
; GENERAL INFORMATION:
; APPLICANT: Lalagudi, Raghunath V.
; APPLICANT: Kamigaki, Laura Y. (Ito)
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
; FILE REFERENCE: PL-0012-1 CON
; CURRENT APPLICATION NUMBER: US/09/923,876
; CURRENT FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: 09/298,329
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/085,331
; PRIOR FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 6332
; SOFTWARE: PERL Program
; SEQ ID NO 1462
; LENGTH: 264
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020013958A1 700158849H1
; NAME/KEY: unsure
; LOCATION: 250, 254, 261, 263
; OTHER INFORMATION: a, t, c, g, or other
US-09-923-876-1462

Query Match          0.9%; Score 17; DB 10; Length 264;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1073 GGTCCTCAGTAATATGCT 1089
      |||
Db 75 GGTCCTCAGTAATATGCT 59

RESULT 8
US-09-960-352-7464
; Sequence 7464, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 7464
; LENGTH: 433
; TYPE: DNA

; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 32-LIB3058-049-Q1-K1-H7
US-09-960-352-7464

Query Match          0.9%; Score 17; DB 10; Length 433;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1625 GACAAAGACTCTGCTGG 1641
      |||
Db 136 GACAAAGACTCTGCTGG 152

RESULT 9
US-09-960-352-4610/c
; Sequence 4610, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengbing
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 4610
; LENGTH: 443
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 20-LIB3058-021-Q1-K1-E7
US-09-960-352-4610

Query Match          0.9%; Score 17; DB 10; Length 443;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 636 TGAAGATTCATTGG 652
      |||
Db 351 TGAAGATTCATTGG 335

RESULT 10
US-09-864-761-2452
; Sequence 2452, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 2462
; LENGTH: 476
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL080243.21
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 12
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 9.7
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 28
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 70
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 16
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.2
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 25
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 55
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 15
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 7.3
US-09-864-761-2462
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Query Match 0.9%; Score 17; DB 10; Length 476;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 864 AGCTGATCGAAGAGTAT 880
Db 24 AGCTGATCGAAGAGTAT 40
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RESULT 11
US-09-864-761-7247/c
; Sequence 7247, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeonica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
```

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; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 7247
; LENGTH: 597
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC015649.5
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.9
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.5
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.6
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.2
US-09-864-761-7247
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Query Match 0.9%; Score 17; DB 10; Length 597;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 1207 GCCATGTCAAAGAACT 1223
Db 375 GCCATGTCAAAGAACT 359
|||||
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```
RESULT 12
US-09-864-761-19193
; Sequence 19193, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeonica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
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; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 19193
; LENGTH: 610
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL080243.21
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 12
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 9.7
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 28
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 70
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 16
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.2
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 25
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 55
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 15
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 7.3
; OTHER INFORMATION: EST.HUMAN HIT: B6795542.1, EVALUE 0.00e+00
; OTHER INFORMATION: NT HIT: g111424380, EVALUE 0.00e+00
; OTHER INFORMATION: SWISSPROT HIT: P29314, EVALUE 8.00e-90
US-09-864-761-19193

Query Match 0.9%; Score 17; DB 10; Length 610;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 864 AGCTGATCGAAGATAT 880
|||||
DB 114 ACCTGATCGAAGATAT 130

RESULT 13
US-09-770-445-714
; Sequence 714, Application US/09770445
; Patent No. US20020023281A1
; GENERAL INFORMATION:
; APPLICANT: Gorlach, Jörn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.

; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Krieker, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE REFERENCE: 2023US (PARA-012PRV)
; CURRENT APPLICATION NUMBER: US/09/770,445
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 60/178,472
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 714
; LENGTH: 826
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-770-445-714

Query Match 0.9%; Score 17; DB 10; Length 826;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 788 AGTCACGACTCCACTT 804
|||||
DB 739 AGTCACGACTCCACTT 755

RESULT 14
US-09-938-842A-4623/C
; Sequence 4623, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SCRI1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,847
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 4623
; LENGTH: 880
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-4623

Query Match 0.9%; Score 17; DB 9; Length 880;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 751 CCACCTTTGTGATGAGAC 767
|||||
DB 47 CCACCTTTGTGATGAGAC 31

RESULT 15
US-09-925-301-134/c
; Sequence 134, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: P4106
; CURRENT APPLICATION NUMBER: US/09/925,301
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 134
; LENGTH: 1657
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-301-134
Query Match 0.9%; Score 17; DB 10; Length 1657;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 719 CTCCTTATGGTGACTCC 735
|||||
Db 1085 CTCCTTATGGTGACTCC 1069

Search completed: November 12, 2002, 07:56:54
JOB time : 85 secs